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(21) International Application Number: PCT/US99/15838 (22) International Filing Date: 14 July 1999 (14.07.99) (30) Priority Data: <table border="0"><tr><td>09/115,453</td><td>14 July 1998 (14.07.98)</td><td>US</td></tr><tr><td>09/116,134</td><td>14 July 1998 (14.07.98)</td><td>US</td></tr><tr><td>09/159,822</td><td>23 September 1998 (23.09.98)</td><td>US</td></tr><tr><td>09/159,812</td><td>23 September 1998 (23.09.98)</td><td>US</td></tr><tr><td>09/232,880</td><td>15 January 1999 (15.01.99)</td><td>US</td></tr><tr><td>09/232,149</td><td>15 January 1999 (15.01.99)</td><td>US</td></tr><tr><td>09/288,946</td><td>9 April 1999 (09.04.99)</td><td>US</td></tr></table> (71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US). (72) Inventors: DILLON, Davin, Clifford; 21607 N.E. 24th Street, Redmond, WA 98053 (US). HARLOCKER, Susan, Louise; 6203 20th Avenue N.W., Seattle, WA 98107 (US). YUQIU, Jiang; 5001 South 232nd Street, Kent, WA 98032 (US). XU, Jiangchun; 15805 S.E. 43rd Place, Bellevue, WA 98006 (US). MITCHAM, Jennifer, Lynn; 16677 Northeast 88th Street, Redmond, WA 98052 (US).		09/115,453	14 July 1998 (14.07.98)	US	09/116,134	14 July 1998 (14.07.98)	US	09/159,822	23 September 1998 (23.09.98)	US	09/159,812	23 September 1998 (23.09.98)	US	09/232,880	15 January 1999 (15.01.99)	US	09/232,149	15 January 1999 (15.01.99)	US	09/288,946	9 April 1999 (09.04.99)	US	(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia, 701 Fifth Avenue, Seattle, WA 98104-7092 (US). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>	
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(54) Title: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER																								
(57) Abstract Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.																								

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COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER

TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present

invention provides polypeptides comprising at least a portion of a prostate tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a tumor protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and a non-specific immune response enhancer.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a non-specific immune response enhancer.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a non-specific immune response enhancer.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited

above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic

kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate tumor polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate tumor polypeptide P502S. In each case, the number of γ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/*neu*.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate tumor polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8⁺ cell line (3A-1) for a representative prostate tumor antigen (P501S). Figure 6A shows the results of a ⁵¹Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12
SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16
SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1
SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9
SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4
SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17
SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17
SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12
SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12
SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862
SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862
SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13
SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13
SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19
SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19
SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25
SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25
SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24
SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24
SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58
SEQ ID NO: 23 is the determined 3' cDNA sequence for K1-58
SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63
SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63
SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4
SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4
SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14
SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14
SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12
SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16
SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21
SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48
SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55
SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2
SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6
SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858
SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864
SEQ ID NO: 41 is the determined cDNA sequence for P5
SEQ ID NO: 42 is the determined cDNA sequence for P8
SEQ ID NO: 43 is the determined cDNA sequence for P9
SEQ ID NO: 44 is the determined cDNA sequence for P18
SEQ ID NO: 45 is the determined cDNA sequence for P20
SEQ ID NO: 46 is the determined cDNA sequence for P29
SEQ ID NO: 47 is the determined cDNA sequence for P30
SEQ ID NO: 48 is the determined cDNA sequence for P34
SEQ ID NO: 49 is the determined cDNA sequence for P36
SEQ ID NO: 50 is the determined cDNA sequence for P38
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SEQ ID NO: 52 is the determined cDNA sequence for P42
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SEQ ID NO: 56 is the determined cDNA sequence for P53
SEQ ID NO: 57 is the determined cDNA sequence for P55
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SEQ ID NO: 59 is the determined cDNA sequence for P64
SEQ ID NO: 60 is the determined cDNA sequence for P65
SEQ ID NO: 61 is the determined cDNA sequence for P73
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SEQ ID NO: 64 is the determined cDNA sequence for P79
SEQ ID NO: 65 is the determined cDNA sequence for P84
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SEQ ID NO: 71 is the determined cDNA sequence for V1-3692
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SEQ ID NO: 73 is the determined cDNA sequence for V1-3686
SEQ ID NO: 74 is the determined cDNA sequence for R1-2330
SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976
SEQ ID NO: 76 is the determined cDNA sequence for V1-3679

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SEQ ID NO: 84 is the determined cDNA sequence for 1H-4785
SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787
SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796
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SEQ ID NO: 88 is the determined cDNA sequence for 1I-4810
SEQ ID NO: 89 is the determined cDNA sequence for 1I-4811
SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876
SEQ ID NO: 91 is the determined cDNA sequence for 1K-4884
SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896
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SEQ ID NO: 108 is the predicted amino acid sequence for F1-12
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SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12
SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862
SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

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SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-4774
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SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-4787

SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-4796
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SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-4762
SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-4766
SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770
SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771
SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-4772
SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-4309
SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278
SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288
SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283
SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304
SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296
SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280
SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd
SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con
SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev
SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd
SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev
SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd
SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev
SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd
SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev
SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd
SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev
SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd
SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev
SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev
SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd
SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev
SEQ ID NO: 223 is the determined cDNA sequence for P509S

SEQ ID NO: 224 is the determined cDNA sequence for P510S
SEQ ID NO: 225 is the determined cDNA sequence for P703DE5
SEQ ID NO: 226 is the determined cDNA sequence for 9-A11
SEQ ID NO: 227 is the determined cDNA sequence for 8-C6
SEQ ID NO: 228 is the determined cDNA sequence for 8-H7
SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13
SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14
SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23
SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24
SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25
SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30
SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35
SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38
SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41
SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42
SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45
SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56
SEQ ID NO: 247 is the determined cDNA sequence for PTPN64
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65
SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84
SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86
SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2
SEQ ID NO: 259 is the determined cDNA sequence for JP1B1
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2

SEQ ID NO: 261 is the determined cDNA sequence for JP1D3
SEQ ID NO: 262 is the determined cDNA sequence for JP1A4
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7
SEQ ID NO: 293 is the determined cDNA sequence for P8D8
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10

SEQ ID NO: 298 is the determined cDNA sequence for JP8C10
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9
SEQ ID NO: 303 is the determined cDNA sequence for JP8C12
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12
SEQ ID NO: 307 is the determined cDNA sequence for P711P
SEQ ID NO: 308 is the determined cDNA sequence for P712P
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23
SEQ ID NO: 310 is the determined cDNA sequence for P774P
SEQ ID NO: 311 is the determined cDNA sequence for P775P
SEQ ID NO: 312 is the determined cDNA sequence for P715P
SEQ ID NO: 313 is the determined cDNA sequence for P710P
SEQ ID NO: 314 is the determined cDNA sequence for P767P
SEQ ID NO: 315 is the determined cDNA sequence for P768P
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5
SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5
SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26
SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26
SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23
SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23
SEQ ID NO: 332 is the determined full length cDNA sequence for P509S
SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)
SEQ ID NO: 334 is the determined cDNA sequence for P714P
SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)
SEQ ID NO: 336 is the predicted amino acid sequence for P705P
SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10
SEQ ID NO: 338 is the amino acid sequence of the peptide p5
SEQ ID NO: 339 is the predicted amino acid sequence of P509S
SEQ ID NO: 340 is the determined cDNA sequence for P778P
SEQ ID NO: 341 is the determined cDNA sequence for P786P
SEQ ID NO: 342 is the determined cDNA sequence for P789P

SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)

SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteosome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

SEQ ID NO: 381 is the determined cDNA sequence for B716P.

SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.

SEQ ID NO: 383 is the predicted amino acid sequence for P711P.

SEQ ID NO: 384 is the cDNA sequence for P1000C.

SEQ ID NO: 385 is the cDNA sequence for CGI-82.

SEQ ID NO:386 is the cDNA sequence for 23320.

SEQ ID NO:387 is the cDNA sequence for CGI-69.

SEQ ID NO:388 is the cDNA sequence for L-iditol-2-dehydrogenase.

SEQ ID NO:389 is the cDNA sequence for 23379.

SEQ ID NO:390 is the cDNA sequence for 23381.

SEQ ID NO:391 is the cDNA sequence for KIAA0122.

SEQ ID NO:392 is the cDNA sequence for 23399.

SEQ ID NO:393 is the cDNA sequence for a previously identified gene.

SEQ ID NO:394 is the cDNA sequence for HCLBP.

SEQ ID NO:395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.

SEQ ID NO:399 is the cDNA sequence for hTGR.

SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

SEQ ID NO:404 is the cDNA sequence for 22550.

SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553.

SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.
SEQ ID NO:415 is the cDNA sequence for 22572.
SEQ ID NO:416 is the cDNA sequence for 22573.
SEQ ID NO:417 is the cDNA sequence for 22573.
SEQ ID NO:418 is the cDNA sequence for 22575.
SEQ ID NO:419 is the cDNA sequence for 22580.
SEQ ID NO:420 is the cDNA sequence for 22581.
SEQ ID NO:421 is the cDNA sequence for 22582.
SEQ ID NO:422 is the cDNA sequence for 22583.
SEQ ID NO:423 is the cDNA sequence for 22584.
SEQ ID NO:424 is the cDNA sequence for 22585.
SEQ ID NO:425 is the cDNA sequence for 22586.
SEQ ID NO:426 is the cDNA sequence for 22587.
SEQ ID NO:427 is the cDNA sequence for 22588.
SEQ ID NO:428 is the cDNA sequence for 22589.
SEQ ID NO:429 is the cDNA sequence for 22590.
SEQ ID NO:430 is the cDNA sequence for 22591.
SEQ ID NO:431 is the cDNA sequence for 22592.
SEQ ID NO:432 is the cDNA sequence for 22593.
SEQ ID NO:433 is the cDNA sequence for 22594.
SEQ ID NO:434 is the cDNA sequence for 22595.
SEQ ID NO:435 is the cDNA sequence for 22596.
SEQ ID NO:436 is the cDNA sequence for 22847.
SEQ ID NO:437 is the cDNA sequence for 22848.
SEQ ID NO:438 is the cDNA sequence for 22849.
SEQ ID NO:439 is the cDNA sequence for 22851.
SEQ ID NO:440 is the cDNA sequence for 22852.
SEQ ID NO:441 is the cDNA sequence for 22853.
SEQ ID NO:442 is the cDNA sequence for 22854.
SEQ ID NO:443 is the cDNA sequence for 22855.
SEQ ID NO:444 is the cDNA sequence for 22856.
SEQ ID NO:445 is the cDNA sequence for 22857.
SEQ ID NO:446 is the cDNA sequence for 23601.
SEQ ID NO:447 is the cDNA sequence for 23602.
SEQ ID NO:448 is the cDNA sequence for 23605.
SEQ ID NO:449 is the cDNA sequence for 23606.
SEQ ID NO:450 is the cDNA sequence for 23612.

SEQ ID NO:451 is the cDNA sequence for 23614.
SEQ ID NO:452 is the cDNA sequence for 23618.
SEQ ID NO:453 is the cDNA sequence for 23622.
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.
SEQ ID NO:455 is the cDNA sequence for LIM protein.
SEQ ID NO:456 is the cDNA sequence for a known gene.
SEQ ID NO:457 is the cDNA sequence for a known gene.
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.
SEQ ID NO:459 is the cDNA sequence for 23045.
SEQ ID NO:460 is the cDNA sequence for 23032.
SEQ ID NO:461 is the cDNA sequence for 23054.
SEQ ID NOs:462-467 are cDNA sequences for known genes.
SEQ ID NOs:468-471 are cDNA sequences for P710P.
SEQ ID NO:472 is a cDNA sequence for P1001C.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate tumor protein or a variant thereof. A "prostate tumor protein" is a protein that is expressed in prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain prostate tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human prostate tumor proteins. Sequences of polynucleotides encoding certain tumor proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Sequences of polypeptides comprising at least a portion of a tumor protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

PROSTATE TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate tumor protein or a portion thereof.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50,

in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenesis pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to

the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, a prostate tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using

standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate tumor protein are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Isolation of these

polynucleotides is described below. Each of these prostate tumor proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such

as inosine, queosine and wybutosine, as well as acetyl-, methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (i.e., an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

PROSTATE TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate tumor protein or a variant thereof, as described herein. As noted above, a "prostate tumor protein" is a protein that is expressed by prostate tumor cells. Proteins that are prostate tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from

the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein.

Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are

E. coli, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into

the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as

amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, urine and/or tumor biopsies) from

patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient

time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and

thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (*see also* U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate tumor polypeptide, polynucleotide encoding a prostate tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience

(Greene 1998)). T cells that have been activated in response to a prostate tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Prostate tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a prostate tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998,

and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or

preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6, IL-10 and TNF- β) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is

quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-

surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a prostate tumor protein (or portion or other variant thereof) such that the prostate tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the prostate tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that

provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein

may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such

a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding

agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred

embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate tumor polypeptides to

detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a prostate tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate tumor polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a prostate tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers

comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375 and 381. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 μ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 μ l of

H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human

autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted

amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO: 73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and

prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA⁺ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that

F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression

in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney). The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated

and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable.

Increased expression of 8-F11 was seen in prostate tumor and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues.

Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350-365.

EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2.1 (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100 μ g of P2S#12 and 120 μ g of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6×10^6 cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2×10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7 μ g/ml dextran sulfate and 25 μ g/ml LPS for 3 days). Six days later, cells (5×10^5 /ml) were restimulated with 2.5×10^6 /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were

restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2.1 expressing) transduced with P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2.1 molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 $\mu\text{g/ml}$ were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2.1 were immunized as described by Theobald *et al.* (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5 μg of P1S #10 and 120 μg of an I-A^b binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at 6×10^6 cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed ($2\mu\text{g/ml}$ P1S#10 and 10mg/ml β 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7 $\mu\text{g/ml}$ dextran sulfate and 25 $\mu\text{g/ml}$ LPS for 3 days). Six days later cells ($5 \times 10^5/\text{ml}$) were restimulated with $2.5 \times 10^6/\text{ml}$ peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and $3 \times 10^6/\text{ml}$ A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly

basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

EXAMPLE 7

ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE TUMOR POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8⁺ T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8⁺ T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a γ -interferon ELISPOT assay (see Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on 10^4 fibroblasts in the presence of 3 μ g/ml human β_2 -microglobulin and 1 μ g/ml P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml γ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of γ -interferon spots with increasing numbers of T

cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

EXAMPLE 8

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate tumor antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 µg VR10132-P501S either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed A2-restricted CTL epitope.

EXAMPLE 9

GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH PROSTATE TUMOR ANTIGEN

Using *in vitro* whole-gene priming with P501S-retrovirally transduced autologous fibroblasts (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon-γ ELISPOT analysis as described above. Using a panel of HLA-mismatched fibroblast lines transduced with P501S, these CTL lines were shown to be restricted HLA-A2 class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 µg/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and

priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S. Following four stimulation cycles, CD8⁺ T cell lines were identified that specifically produced interferon- γ when stimulated with P501S-transduced autologous fibroblasts. The P501S-specific activity could be sustained by the continued stimulation of the cultures with P501S-transduced fibroblasts in the presence of IL-15. A panel of HLA-mismatched fibroblast lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- γ in an ELISPOT assay, the P501S specific response was shown to be restricted by HLA-A2. These results demonstrate that a CD8⁺ CTL response to P501S can be elicited.

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN A PROSTATE TUMOR ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific CD8⁺ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2 transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of P703P transduced target cells expressing either HLA-A2Kb or HLA-A2. Specifically, HLA-A2 transgenic mice were immunized subcutaneously in the footpad with 100 μ g of p5 peptide together with 140 μ g of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with p5 peptide and cultured with GM-CSF and IL-4 together with CD8⁺ T cell enriched PBMC. CTL lines were restimulated on a weekly basis

with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures, CTL recognition of p5-pulsed target cells was demonstrated.

EXAMPLE 11

EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate tumor and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach).

EXAMPLE 12

ELICITATION OF PROSTATE TUMOR ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate tumor antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GMCSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8⁺ cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles, CD8⁺ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to

express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (^{51}Cr release) and interferon-gamma production (Interferon-gamma Elispot; *see above* and Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

EXAMPLE 13

IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

Table I
Summary of Prostate Tumor Antigens

Known Genes	Previously identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang(23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	

transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate

tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

EXAMPLE 14

IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate tumor antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups, Plus (normal prostate and prostate tumor libraries, and breast cell lines, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II
Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones found in the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones found in the Plus, Minus and Other group libraries, but the expression in the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones found in Plus, Minus and Other group libraries, but the expression in the Plus group is higher than the expression in the Minus group. This analysis identified 4,345 breast clusters (*see* Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor cDNA was at least three times the level in normal prostate cDNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NOs:401-453, with certain novel sequences shown in SEQ ID NOs:407, 413, 416-419, 422, 426, 427 and 450.

Table IV
Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P

403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57

439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

EXAMPLE 15

FURTHER IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NOs:454-467. Of these sequences SEQ ID NOs:459-461 correspond to novel genes. The others (SEQ ID NOs:454-458 and 461-467) correspond to known sequences.

EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE TUMOR ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic ABI Sequencer. Four sequences were obtained, and are presented in SEQ ID NOs:468-471.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339 and 383.

4. An isolated polynucleotide encoding at least 15 amino acid residues of a prostate tumor protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434,

435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

7. An isolated polynucleotide comprising a sequence that hybridizes, under moderately stringent conditions, to a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-7.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An expression vector comprising a polynucleotide according claim 8.

12. A host cell transformed or transfected with an expression vector according to claim 11.

13. A pharmaceutical composition comprising a polypeptide according to claim 1, in combination with a physiologically acceptable carrier.

14. A vaccine comprising a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

15. A vaccine according to claim 14, wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine according to claim 14, wherein the non-specific immune response enhancer induces a predominantly Type I response.

17. A pharmaceutical composition comprising a polynucleotide according to claim 4, in combination with a physiologically acceptable carrier.

18. A vaccine comprising a polynucleotide according to claim 4, in combination with a non-specific immune response enhancer.

19. A vaccine according to claim 18, wherein the non-specific immune response enhancer is an adjuvant.

20. A vaccine according to claim 18, wherein the non-specific immune response enhancer induces a predominantly Type I response.

21. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472 or a complement of any of the foregoing polynucleotide sequences.

22. A pharmaceutical composition comprising an antibody or fragment thereof according to claim 18, in combination with a physiologically acceptable carrier.
23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.
24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.
25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.
26. A vaccine according to claim 25, wherein the non-specific immune response enhancer is an adjuvant.
27. A vaccine according to claim 25, wherein the non-specific immune response enhancer induces a predominantly Type I response.
28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.
29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.
30. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polynucleotide according to claim 4, and thereby inhibiting the development of a cancer in the patient.
31. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antibody or antigen-binding fragment thereof according to claim 21, and thereby inhibiting the development of a cancer in the patient.

32. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

33. A method according to claim 32, wherein the antigen-presenting cell is a dendritic cell.

34. A method according to any one of claims 29-32, wherein the cancer is prostate cancer.

35. A fusion protein comprising at least one polypeptide according to claim 1.

36. A fusion protein according to claim 35, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

37. A fusion protein according to claim 35, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

38. A fusion protein according to claim 35, wherein the fusion protein comprises an affinity tag.

39. An isolated polynucleotide encoding a fusion protein according to claim 35.

40. A pharmaceutical composition comprising a fusion protein according to claim 32, in combination with a physiologically acceptable carrier.

41. A vaccine comprising a fusion protein according to claim 35, in combination with a non-specific immune response enhancer.

42. A vaccine according to claim 41, wherein the non-specific immune response enhancer is an adjuvant.

43. A vaccine according to claim 41, wherein the non-specific immune response enhancer induces a predominantly Type I response.
44. A pharmaceutical composition comprising a polynucleotide according to claim 40, in combination with a physiologically acceptable carrier.
45. A vaccine comprising a polynucleotide according to claim 40, in combination with a non-specific immune response enhancer.
46. A vaccine according to claim 45, wherein the non-specific immune response enhancer is an adjuvant.
47. A vaccine according to claim 45, wherein the non-specific immune response enhancer induces a predominantly Type I response.
48. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 40 or claim 44.
49. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 41 or claim 45.
50. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
- (i) polynucleotides recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and
 - (ii) complements of the foregoing polynucleotides;
- wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate tumor protein from the sample.
51. A method according to claim 50, wherein the biological sample is blood or a fraction thereof.

52. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

53. A method for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of:

- (i) a polypeptide according to claim 1;
 - (ii) a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
 - (iii) a polynucleotide encoding a polypeptide of (i) or (ii); and/or
 - (iv) an antigen presenting cell that expresses a polypeptide of (i) or (ii);
- under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

54. An isolated T cell population, comprising T cells prepared according to the method of claim 53.

55. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 54.

56. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

- (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:
 - (i) a polypeptide according to claim 1;
 - (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
 - (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
 - (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

- (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

57. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) a polypeptide according to claim 1;
- (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
- (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
- (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate;

- (b) cloning at least one proliferated cell; and
- (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

58. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

- (ii) complements of the foregoing polynucleotides;
- (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

59. A method according to claim 58, wherein the binding agent is an antibody.

60. A method according to claim 59, wherein the antibody is a monoclonal antibody.

61. A method according to claim 58, wherein the cancer is prostate cancer.
62. A method for monitoring the progression of a cancer in a patient, comprising the steps of:
- (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;
 - (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
 - (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
 - (d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.
63. A method according to claim 62, wherein the binding agent is an antibody.
64. A method according to claim 63, wherein the antibody is a monoclonal antibody.
65. A method according to claim 62, wherein the cancer is a prostate cancer.
66. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:
- (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;
 - (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

67. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

68. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

69. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

70. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

71. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

72. A diagnostic kit, comprising:

- (a) one or more antibodies according to claim 21; and
- (b) a detection reagent comprising a reporter group.

73. A kit according to claim 72, wherein the antibodies are immobilized on a solid support.

74. A kit according to claim 73, wherein the solid support comprises nitrocellulose, latex or a plastic material.

75. A kit according to claim 72, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

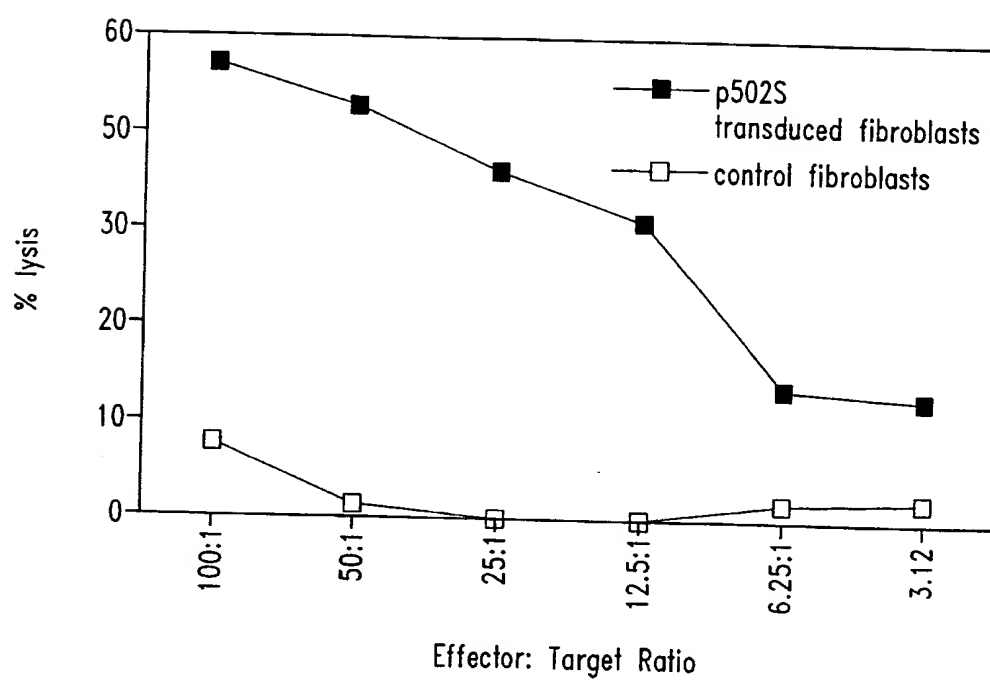
76. A kit according to claim 72, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

77. An oligonucleotide comprising 10 to 40 nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotides.

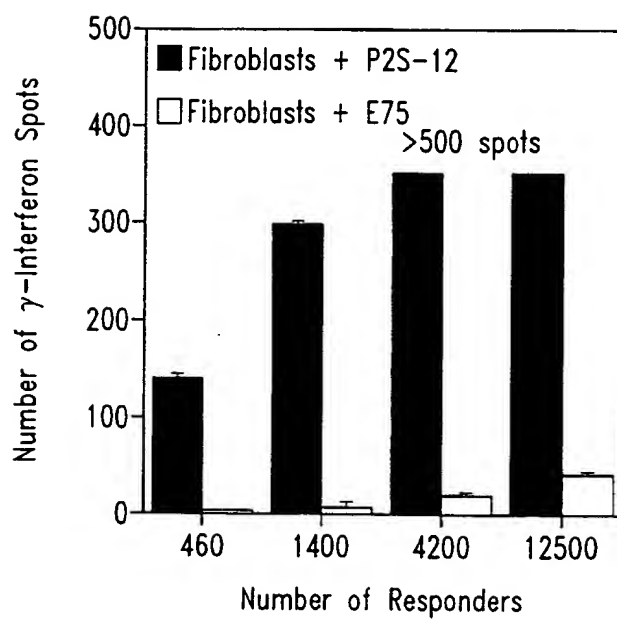
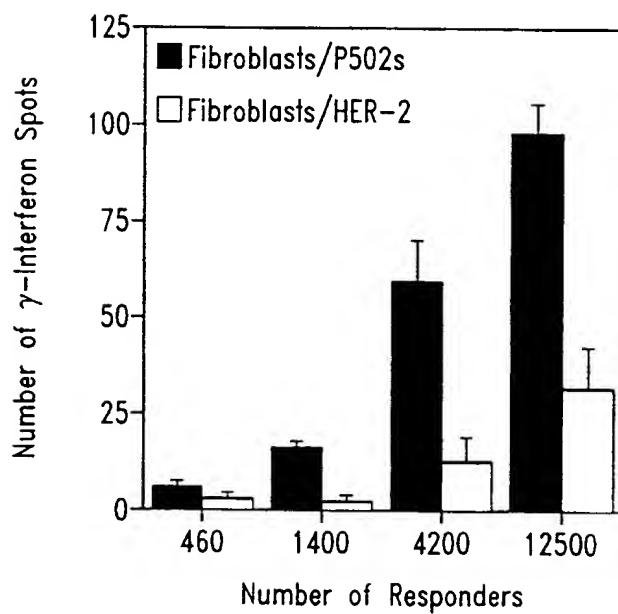
78. A oligonucleotide according to claim 77, wherein the oligonucleotide comprises 10-40 nucleotides recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

79. A diagnostic kit, comprising:
(a) an oligonucleotide according to claim 77; and
(b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

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*Fig. 1*

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*Fig. 2A**Fig. 2B*

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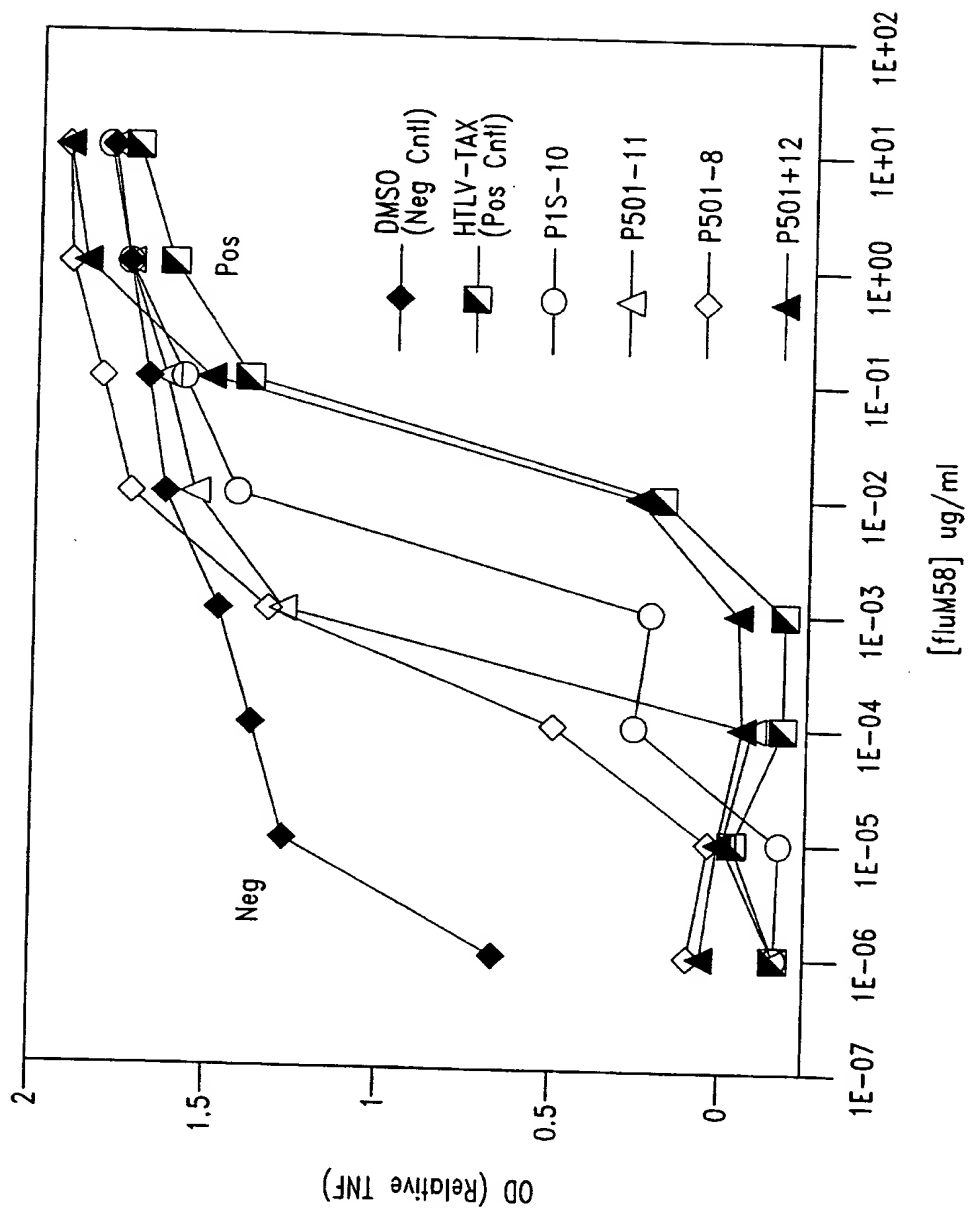
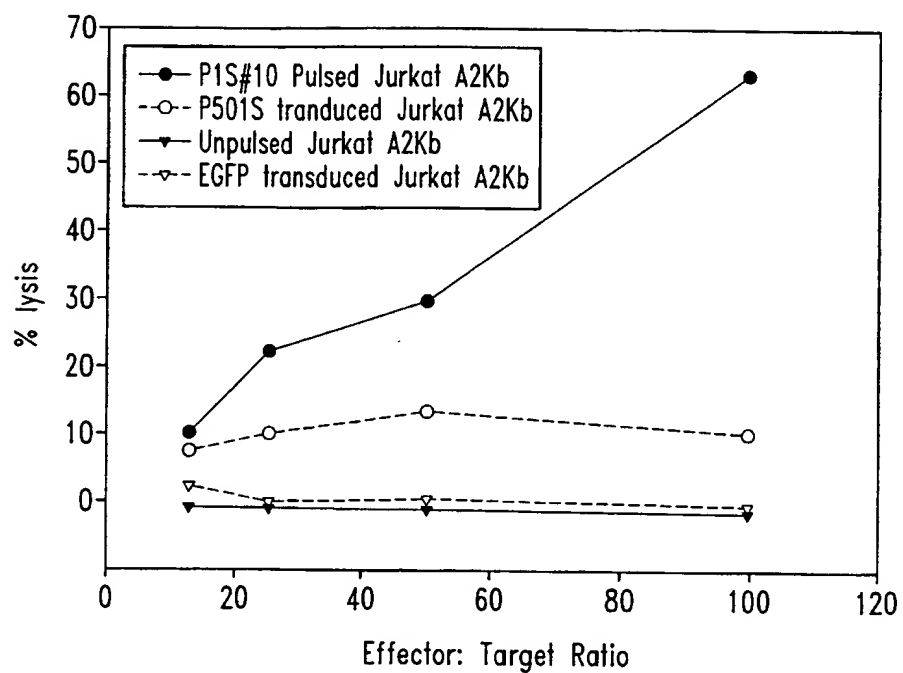
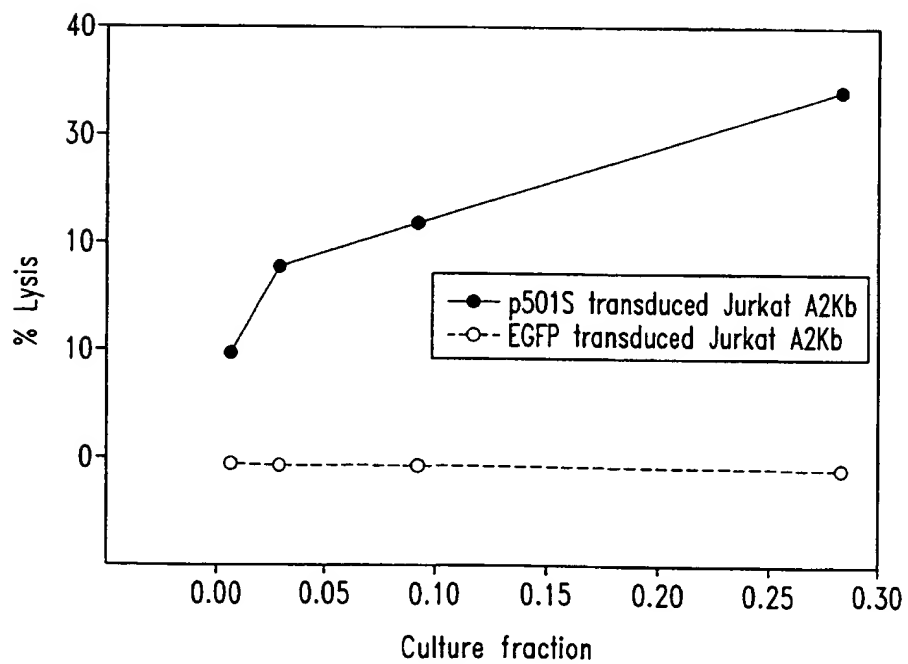
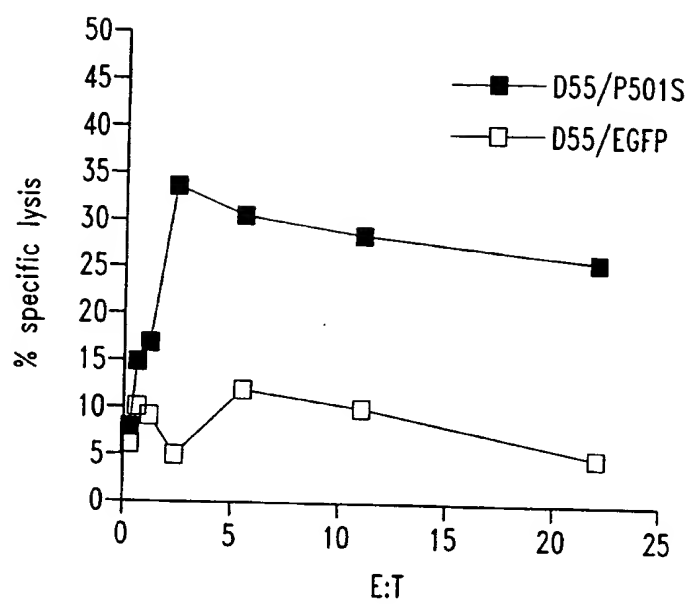
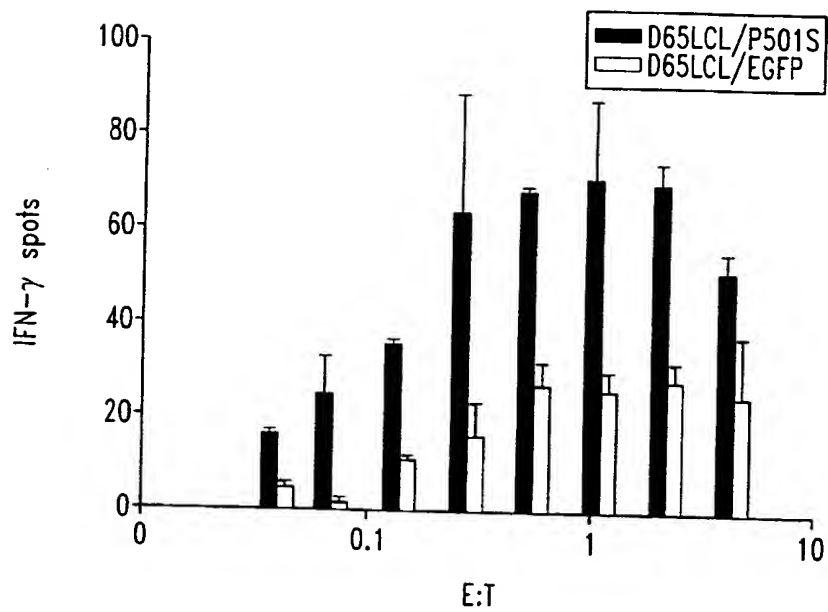


Fig. 3

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*Fig. 4**Fig. 5*

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*Fig. 6**Fig. 7*

SEQUENCE LISTING

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tctgccttcg tcttctttgc aaatacatct gcaaacttct tcttcatttc tggccaatca      240
tccatgctca tctgattggg aagttcatca gactttagtc canntccttt gatcagcagc      300
tcgtagaact ggggttctat tgctccaaca gccatgaatt ccccatctgc tgtcctgtaa      360
gtcgtataga aaggtgctcc accatccaac atgttctgtc ctgcaggggg ggcccggtag      420
ccaattcgcc ctatantgag tcgtattacg cgcgctcact ggccgtcgtt ttacaacgtc      480
gtgactggga aaaccctggg cgttaccaac ttaatcgctt tgcagcacat cccctttcgc      540
ccagctgggc gtaatancca aaaggcccgc accgatcgcc cttccaacag ttgcgcacct      600
gaatgggnaa atgggacccc cctgttacgg cgcattnaac ccccgcnagg tttngttgtt      660
acccccacnt nnaccgctta cactttgcca gcgccttanc gcccgctccc tttcnctttt      720
cttcccttcc tttcnncncc ctttcccccg ggggtttcccc cntcaaacc cna                                773

```

<210> 4

<211> 828

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(828)

<223> n = A,T,C or G

<400> 4

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cctcctgagt cctactgacc tgtgctttct ggtgtggagt ccagggtgctc taggaaaagg      60
aatgggcaga cacaggtgta tgccaatgtt tctgaaatgg gtataatttc gtccctctcct      120
tcggaacact ggctgtctct gaagacttct cgctcagttt cagtgaggac acacacaaag      180
acgtgggtga ccatgttggt tgtggggtgc agagatggga ggggtggggc ccaccctgga      240
agagtggaca gtgacacaag gtggacactc tctacagatc actgaggata agctggagcc      300
acaatgcacg aggcacacac acagcaagga tgacnctgta aacatagccc acgctgtcct      360

```

```

gnngggcactg ggaagcctan atnaggccgt gagcanaaag aaggggagga tccactagtt      420
ctanagcggc cgccaccgcg gtgganctcc ancttttgtt cccttttagtg aggggttaatt      480
gcgcgcttg chtaactcatg gtcatanctn tttcctgtgt gaaattgtta tccgctcaca      540
attccacaca acatacganc cggaacata aantgtaaac ctgggggtgcc taatgantga      600
ctaactcaca ttaattgctg tgcgctcact gcccgtttc caatcnggaa acctgtcttg      660
ccncttgcat tnatgaatcn gccaaccccc ggggaaaagc gtttgcgttt tgggcgctct      720
tccgcttcct cnetcantta ntccctncnc tcggtcattc cggctgcngc aaaccgggtc      780
accnctcca aaggggggtat tccggtttcc ccnaatccgg gganancc      828

```

<210> 5

<211> 834

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(834)

<223> n = A,T,C or G

<400> 5

```

tttttttttt tttttactga tagatggaat ttattaagct tttcacatgt gatagcacat      60
agttttaatt gcatccaaag tactaacaaa aactctagca atcaagaatg gcagcatggt      120
attttataac aatcaacacc tgtggctttt aaaatttggg tttcataaga taattttatac      180
tgaagttaat ctagccatgc ttttaaaaaa tgcttttagg cactccaagc ttggcagtta      240
acatttgcca taaacaataa taaaacaatc acaatttaat aaataacaaa tacaacattg      300
taggccataa tcatatacag tataaggaaa aggtggtagt gttgagtaag cagttattag      360
aatagaatac cttggcctct atgcaaatat gtctagacac tttgattcac tcagccctga      420
cattcagttt tcaaagtagg agacagggtc tacagtatca ttttacagtt tccaacacat      480
tgaaaacaag tagaaaatga tgagttgatt ttattaatg cattacatcc tcaagagtta      540
tcaccaaccc ctcagttata aaaaattttc aagttatatt agtcatataa cttggtgtgc      600
ttatttttaa ttagtgctaa atggattaag tgaagacaac aatggtcccc taatgtgatt      660
gatattggtc atttttacca gcttctaaat ctnaactttc aggcctttga actggaacat      720
tgnatnacag tgttccanag ttncaaccta ctggaacatt acagtgtgct tgattcaaaa      780
tgttattttg ttaaaaatta aattttaacc tgggtggaaa ataatttgaa atna      834

```

<210> 6

<211> 818

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(818)

<223> n = A,T,C or G

<400> 6

```

tttttttttt tttttttttt aagaccctca tcaatagatg gagacatata gaaatagtca      60
aaccacatct acaaaatgcc agtatcaggc ggcggtctcg aagccaaagt gatgtttgga      120
tgtaaaagtga aatattagtt ggcggatgaa gcagatagtg aggaaagtgt agccaataat      180
gacgtgaagt ccgtggaagc ctgtggctac aaaaaatgtt gagccgtaga tgccgtcgga      240
aatggtgaag ggagactcga agtactctga ggctttagg agggtaaaat agagaccacg      300
taaaattgta ataaagcagtg ctgaattat ttggtttcgg ttgttttcta ttagactatg      360
gtgagctcag gtgattgata ctcctgatgc gagtaatacg gatgtgttta ggagtgggac      420
ttctagggga tttagcgggg tgatgcctgt tgggggccag tgccctccta gttggggggg      480
aggggctagg ctggagtggg aaaaaggctc gaaaaatcct gcgaagaaaa aaacttctga      540

```

```

ggtaataaat aggattatcc cgtatcgaag gccttttttg acagggtggtg tgtggtggcc      600
ttggtatgtg ctttctcgtg ttacatcgcg ccatcattgg tatatggtta gtgtgttggg      660
ttantanggc ctantatgaa gaacttttgg antggaatta aatcaatngc ttggccggaa      720
gtcattanga nggctnaaaa ggccctgtta nnggtctggg ctnggtttta cccnaccat      780
ggaatncncc ccccggaacna ntgnatccct attcttaa      818

```

```

<210> 7
<211> 817
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(817)
<223> n = A,T,C or G

```

```

<400> 7
tttttttttt tttttttttt tggctctaga gggggtagag ggggtgctat agggtaaata      60
cgggccctat ttcaaagatt tttaggggaa ttaattctag gacgatgggt atgaaactgt      120
ggtttgctcc acagatttca gagcattgac cgtagtatac ccccggtcgt gtagcgggtga      180
aagtggtttg gtttagacgt ccgggaattg catctgtttt taagcctaata gtggggacag      240
ctcatgagtg caagacgtct tgtgatgtaa ttattatacn aatgggggct tcaatcggga      300
gtactactcg attgtcaacg tcaaggagtc gcaggtcgcc tggttctagg aataatgggg      360
gaagtatgta ggaattgaag attaatccgc cgtagtcggt gttctcctag gttcaatacc      420
attggtggcc aattgatttg atggtaaggg gagggatcgt tgaactcgtc tgttatgtaa      480
aggatncctt ngggatggga aggcnatnaa ggactangga tnaatggcgg gcangatatt      540
tcaaacngtc tctanttcct gaaacgtctg aaatgttaat aanaattaan tttngttatt      600
gaatnttng gaaaagggtc tacaggacta gaaaccaaata angaaaanta atnntaangg      660
cnttatcntn aaaggnata accnctccta tnatcccacc caatngnatt cccacnenn      720
acnattggat nccccanttc canaaanggc cccccccggg tgnannccnc cttttgttcc      780
cttnantgan ggttattcnc cctngcntt atcance      818

```

```

<210> 8
<211> 799
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(799)
<223> n = A,T,C or G

```

```

<400> 8
catttcggg tttactttct aaggaaagcc gagcggagc tgctaactgt ggaatcgggt      60
cataaggaga actttctgct ggcacgcgct agggacaagc gggagagcga ctccgagcgt      120
ctgaagcgca cgtcccagaa ggtggacttg gcaactgaaac agctgggaca catccgcgag      180
tacgaacagc gctgaaagt gctggagcgg gaggtccagc agtgtagccg cgtcctgggg      240
tgggtggccg angcctganc cgctctgcct tgctgcccc angtgggccg ccacccctg      300
acctgcctgg gtccaaacac tgagccctgc tggcgactt caagganaac cccacangg      360
ggattttgct cctanantaa ggctcatctg ggccctcgcc cccccacctg gttggccttg      420
tctttgagnt gagcccatg tccatctggg ccaactgtcng gaccaccttt nggagtggt      480
ctccttacaa ccacannatg cccggtcct cccggaaacc antcccance tnggaaggat      540
caagnccctn atccactnnt nctanaaccg gccnccnccg cngtggaaacc cnccttntgt      600
tccttttctn tnagggttaa tnnccgcttg gcctnccan ngctcctnnc ntttccnnt      660
gttnaaattg ttangcnccc nccnntcccn cncnncnann cccgaccenn annttnnann      720

```

ncctgggggt ncnncngat tgaccnnc nccctntant tgcnttnggg ncnntgccc 780
ctttccctct nggganncg 799

<210> 9

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(801)

<223> n = A,T,C or G

<400> 9

acgccttgat cctcccaggc tgggactggt tctgggagga gccgggcatg ctgtggtttg	60
taangatgac actcccaaag gtggtcctga cagtggccca gatggacatg gggctcacct	120
caaggacaag gccaccaggt gcgggggccc aagcccatat gatccttact ctatgagcaa	180
aatcccctgt gggggcttct ccttgaagtc cgccancagg gctcagtctt tggaccang	240
caggtcatgg ggttgtnnc caactgggg ccncaacgca aaanggcnaa gggcctcngn	300
caccatccc angacgcggc tacactnctg gacctccnc tccaccactt tcatgcgctg	360
ttcntaccg cgnatntgtc ccantgttt cngtgcncac tccancttct nggacgtgcg	420
ctacatacgc cggantcnc nctcccgtt tgtccctatc cagtnccan caacaaattt	480
cncntantg caccnattec cacttttnc agntttcnc nncngcttc cttntaaaag	540
ggttganccc cggaaaatnc cccaaagggg gggggcngg tacccaaactn cccctnata	600
gctgaantcc ccatnaccnn gnctnatgg anccntccnt ttaannacn ttctnaactt	660
gggaananc ctcgncntn ccccnttaa tccnccctg cnangnncnt ccccnntcc	720
nccnnntng gcntntnann cnaaaaaggc ccnnnancaa tctcctnncn cctcanttcg	780
ccanccctcg aaatcgccn c	801

<210> 10

<211> 789

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(789)

<223> n = A,T,C or G

<400> 10

cagtctatnt ggccagtgtg gcagctttcc ctgtggctgc cggtgccaca tgcctgtccc	60
acagtgtggc cgtggtgaca gcttcagccg cctcaccgg gttcaccttc tcagccctgc	120
agatcctgcc ctacacactg gcctccctct accaccggga gaagcagggtg ttccctgccca	180
aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttcctgc	240
caggccctaa gcctggagct ccctcccta atggacacgt ggggtgctgga ggcagtggcc	300
tgctccacc tccaccgcg ctctgcggg cctctgcctg tgatgtctcc gtacgtgtgg	360
tgggtgggtga gccaccgan gccagggtgg ttccgggccc gggcatctgc ctggacctcg	420
ccatcctgga tagtgcttcc tgctgtccca ngtggcccca tccctgttta tgggtccat	480
tgtccagctc agccagtctg tctactgccta tatggtgtct gccgcaggcc tgggtctggt	540
cccatttact ttgtacaca ggtantattt gacaagaacg anttgccaa atactcagcg	600
ttaaaaaatt ccagcaacat tgggggtgga aggctgcct cactgggtcc aactccccgc	660
tcctgttaac cccatggggc tgccggcttg gccgccaatt tctgttgctg ccaaantnat	720
gtggctctct gctgccacct gttgctggct gaagtgcnta cngcncantc nggggggtng	780
gnggttccc	789

<210> 11
<211> 772
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(772)
<223> n = A,T,C or G

<400> 11
cccacccctac ccaaatatta gacaccaaca cagaaaagct agcaatggat tcccttctac 60
tttggttaaat aaataagtta aatatTTTaaa tgcctgtgtc tctgtgatgg caacagaagg 120
accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc 180
tgtgggctga ggggacctgg ttcttgtgtg ttgccccca ggactcttcc cctacaaata 240
actttcatat gttcaaatec catggaggag tgtttcatcc tagaaactcc catgcaagag 300
ctacattaaa cgaagctgca ggttaagggg cttanagatg ggaaaccagg tgactgagtt 360
tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc 420
ctgagcctgg gtaateccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc 480
ctccctgtat aagtccagac tgaaccccc ttggaaggnc tccagtcagg cagccctana 540
aactggggaa aaaagaaaag gacgccccan cccccagctg tgcanctacg cacctcaaca 600
gcacaggggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaact ngggggggca 660
accccgccac ccnangggg gttaacagga ancngggnaa cntggaaccc aattnaggca 720
ggcccncac ccnaatntt gctgggaaat ttttctctcc ctaaattntt tc 772

<210> 12
<211> 751
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(751)
<223> n = A,T,C or G

<400> 12
gccccattc cagctgccac accaccacg gtgactgcat tagttcggat gtcatacaaaa 60
agctgattga agcaaccctc tactttttgg tcgtgagcct tttgcttggg gcagggtttca 120
ttggctgtgt tggtagcgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180
aagtanggtg agtctcaaa atccgtatag ttggtgaagc cacagcactt gagcccttcc 240
atgggtggtg tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca 300
ggcactacca gcaacgtcag ggaagtgtc agccattgtg gtgtacacca aggcgaccac 360
agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc 420
acacttgctc tcagtcttan caccatanca gcccntgaaa accaananca aagaccacna 480
cnccggctgc gatgaagaaa tnaccccneg ttgacaaact tgcattggcag tggganccac 540
agtggcccna aaaatcttca aaaaggatgc cccatcnatt gaccccccaa atgcccactg 600
ccaacagggg ctgccccacn cncnnaacga tganccnatt gnacaagatc tncntggtct 660
tnatnaacnt gaacctgcn tngtggctcc tgttcaggnc cnnggcctga cttctnaann 720
aangaactcn gaagncccca cngganann g 751

<210> 13
<211> 729
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(729)

<223> n = A,T,C or G

<400> 13

gagccaggcg	tccctctgcc	tgcccaactca	gtggcaacac	ccgggagctg	ttttgtcctt	60
tgtggancct	cagcagtncc	ctctttcaga	actcantgcc	aaganccctg	aacaggagcc	120
accatgcagt	gcttcagctt	cattaagacc	atgatgatcc	tcttcaattt	gctcatcttt	180
ctgtgtggtg	cagccctggt	ggcagtgggc	atctgggtgt	caatcgatgg	ggcatccttt	240
ctgaagatct	tcgggccact	gtcgtccagt	gccatgcagt	ttgtcaacgt	gggctacttc	300
ctcatcgtag	ccggcggtgt	ggtcttagct	ctagggttcc	tgggctgcta	tgggtctaag	360
actgagagca	agtgtgccct	cgtgacgttc	ttcttcaccc	tcctcctcat	cttcattgct	420
gagggttgcaa	tgtgtggtgc	gccttggtgt	acaccacaat	ggctgagcac	ttcctgacgt	480
tgtgtgtaat	gcctgccatc	aanaaaagat	tatgggttcc	caggaanact	tcactcaagt	540
ggttgaacac	caccatgaaa	gggctcaagt	gctgtggctt	cnccaacta	tacggatttt	600
gaagantcac	ctacttcaaa	gaaaanagtg	cctttccccc	atttctgttg	caattgacaa	660
acgtccccaa	cacagccaat	tgaaaacctg	cacccaaccc	aaanggggtc	ccaaccanaa	720
attnaaggg						729

<210> 14

<211> 816

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(816)

<223> n = A,T,C or G

<400> 14

tgtctcttct	caaagtgtgt	cttggtgcc	taacaaccac	cataggtaaa	gcgggagcag	60
tgttcgctga	aggggttgta	gtaccagcgc	gggatgctct	ccttgacagag	tcctgtgtct	120
ggcaggtcca	cgcagtcccc	tttgtcactg	gggaaatgga	tgcgctggag	ctcgtcaaag	180
ccactcgtgt	atttttcaca	ggcagcctcg	tcgcagcgcg	cggggcagtt	gggggtgtct	240
tcacactcca	ggaaactgtc	natgcagcag	ccattgctgc	agcggaaactg	ggtgggctga	300
cangtgccag	agcacactgg	atggcgccct	tccatgnnan	gggccctgng	ggaaagtccc	360
tganccccc	anctgcctct	caaangcccc	accttgacac	ccccgacagg	ctagaatgga	420
atcttcttcc	cgaaggttag	ttnttcttgt	tgcccanc	ancccntaa	acaaactctt	480
gcanatctgc	tccngggggg	tcntantacc	ancgtgggaa	aagaacccca	ggcngcgaa	540
caancttggt	tggatncgaa	gcnataatct	nctnttctgc	ttggtggaca	gcaccantna	600
ctgtnnanct	ttagnccntg	gtcctcntgg	gttgnncttg	aacctaatcn	ccnntcaact	660
gggacaaggt	aantngccnt	cctttnaatt	cccnancntn	ccccctgggt	tgggggtttt	720
cncnctccta	ccccagaaan	nccgtgttcc	cccccaacta	ggggccnaaa	ccnnttnttc	780
cacaacctn	ccccaccac	gggttcngnt	ggttng			816

<210> 15

<211> 783

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(783)

<223> n = A,T,C or G

<400> 15

ccaaggcctg ggcaggcata nacttgaagg tacaacccca ggaaccctg gtgctgaagg	60
atgtggaaaa cacagattgg cgcctactgc ggggtgacac ggatgtcagg gtagagagga	120
aagacccaaa ccaggtggaa ctgtggggac tcaaggaang cacctacctg ttccagctga	180
cagtgactag ctgagaccac ccagaggaca cggccaacgt cacagtcaact gtgctgtcca	240
ccaagcagac agaagactac tgcctcgcac ccaacaangt gggtcgctgc cggggctctt	300
tcccacgctg gtactatgac cccacggagc agatctgcaa gaggttcggt tatggaggct	360
gcttgggcaa caagaacaac taccttcggg aagaagagtg cattctancc tgcnggggtg	420
tgcaagggtg gcctttgana ngcanctctg gggctcangc gactttcccc cagggccctt	480
ccatggaaa ggcacatcca ntgttctctg gcacctgtca gcccaccag ttccgctgca	540
ncaatggctg ctgcatcnac antttcctng aattgtgaca acacccccca ntgccccaa	600
ccctcccaac aaagcttccc tgttnaaaaa tacnccantt ggcttttnac aaacncccg	660
cncctcctt ttcccnntn aacaaagggc nctngcctt gaactgccc aaccnnggaa	720
tctnccnngg aaaaantncc cccctgggt cctnnaance cctccncaa anctncccc	780
ccc	783

<210> 16

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(801)

<223> n = A,T,C or G

<400> 16

gccccaatc cagctgccac accaccacg gtgactgcat tagttcggat gtcatacaaa	60
agctgattga agcaaccctc tacttttttg tcgtgagcct ttgcttggg gcaggtttca	120
ttggctgtgt tggtagctt gtcattgcaa cagaatgggg gaaaggcact gttctctttg	180
aagtaggggt agtcctcaa atccgtatag ttggtagaag cacagcactt gagccctttc	240
atgggtgggt tccacacttg agtgaagtct tctgggaac cataatcttt ctgatggca	300
ggcactacca gcaacgtcag gaagtgtca gccattgttg tgtacaccaa ggcgaccaca	360
gcagctgcaa cctcagcaat gaagatgagg aggaggatga agaagaacgt cncgagggca	420
cacttgctct ccgtcttagc accatagcag cccangaaac caagagcaaa gaccacaacg	480
cnngctgcga atgaaagaaa ntaccacgt tgacaaactg catggccact ggacgacagt	540
tggcccgaa atcttcagaa aagggatgcc ccattgattg aacacccana tgccactgc	600
cnacagggct gcncncncn gaaagaatga gccattgaag aaggatctc ntggctctta	660
tgaactgaaa cntgcatgg tggccctgt tcagggtct tggcagtgaa ttctganaaa	720
aaggaacngc nttagcccc ccaaangana aaacaccccc ggggtgttgc ctgaattggc	780
ggccaaggan ccctgccccn g	801

<210> 17

<211> 740

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(740)

<223> n = A,T,C or G

<400> 17

gtgagagcca ggcgtccctc tgcctgccca ctgagtgga acaccggga gctgttttgt	60
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cctttgtgga	gcctcagcag	ttccctcttt	cagaactcac	tgccaagagc	cctgaacagg	120
agccaccatg	cagtgttca	gcttcattaa	gaccatgatg	atcctcttca	atttgctcat	180
ctttctgtgt	ggtgcagccc	tggtggcagt	gggcatctgg	gtgtcaatcg	atggggcatc	240
ctttctgaag	atcttcgggc	cactgtcgtc	cagtgccatg	cagtttgtca	acgtgggcta	300
cttcctcatc	gcagccggcg	ttgtggtctt	tgctcttggg	ttcctgggct	gctatggtgc	360
taagacggag	agcaagtgtg	ccctcgtgac	gttcttcttc	atcctcctcc	tcattcttcat	420
tgctgaagtt	gcagctgctg	tggtcgcctt	gggtacacac	acaatggctg	aaccattcct	480
gacgttgctg	gtantgcctg	ccatcaanaa	agattatggg	ttcccaggaa	aaattcactc	540
aantntggaa	caccnccatg	aaaagggctc	caatttctgn	tggcttcccc	aactataccg	600
gaattttgaa	agantcncct	tacttccaaa	aaaaaanant	tgcccttncc	cccnttctgt	660
tgcaatgaaa	acntcccaan	acngccaatn	aaaacctgcc	cnnncaaaaa	ggntcncaaa	720
caaaaaaant	nnaagggttn					740

<210> 18

<211> 802

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(802)

<223> n = A,T,C or G

<400> 18

ccgctgggtg	cgctgggtcca	gngnagccac	gaagcacgtc	agcatcacaca	gcctcaatca	60
caaggtcttc	cagctgccgc	acattacgca	gggcaagagc	ctccagcaac	actgcatatg	120
ggatacactt	tacttttagca	gccaggggtga	caactgagag	gtgtcgaagc	ttattcttct	180
gagcctctgt	tagtggagga	agattccggg	cttcagctaa	gtagtacagc	tatgtcccat	240
aagcaaacac	tgtgagcagc	cgaagggtag	aggcaaagtc	actctcagcc	agctctctaa	300
cattggggcat	gtccagcagt	tctccaaaca	cgtagacacc	agnggcctcc	agcacctgat	360
ggatgagtgt	ggccagcgct	gcccccttgg	ccgacttggc	taggagcaga	aattgctcct	420
ggttctgccc	tgtcaccttc	acttccgcac	tcactactgc	actgagtgtg	ggggacttgg	480
gctcaggatg	tccagagacg	tggttccgcc	ccctcnctta	atgacaccgn	ccanncaacc	540
gtcgggtccc	gccgantgng	ttcgtcgtnc	ctgggtcagg	gtctgctggc	cnctacttgc	600
aancttcgtc	nggccccatg	aattcaccnc	accggaactn	gtangatcca	ctnnttctat	660
aaccggncgc	caccgcnnnt	ggaactccac	tcttnttncc	tttacttgag	ggtaagggtc	720
acccttnncc	ttaccttggt	ccaaacctn	cctgtgtctg	anatngtnaa	tcnggncna	780
tnccanccnc	atangaagcc	ng				802

<210> 19

<211> 731

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 19

cnaagcttcc	aggtnacggg	ccgcnaancc	tgaccnagg	tancanaang	cagnncngcg	60
gagcccaccg	tcacngngng	gngtctttat	nggagggggc	ggagccacat	cnctggacnt	120
cntgacccca	actccccncc	ncncantgca	gtgatgagtg	cagaactgaa	ggtnacgtgg	180
caggaaccaa	gancaaannc	tgctccnntc	caagtcggcn	nagggggcg	ggctggccac	240
gcncatccnt	cnagtgtctn	aaagccccnn	cctgtctact	tgtttgaga	acngcnngga	300

```

catgcccagn gttanataac nggcngagag tnanntttgcc tctcccttcc ggctgcgcan 360
cngtntgtct tagnggacat aacctgacta cttaactgaa cccnngaatt tncnccccct 420
ccactaagct cagaacaaaa aacttcgaca ccactcantt gtcacctgnc tgctcaagta 480
aagtgtaccc catncccaat gtntgtctnga ngctctgncc tgcnttangt tgggtcctgg 540
gaagacctat caattnaagc tatgtttctg actgcctctt gtcacctgna acaancnacc 600
cnnnntcca agggggggnc ggcccccaat ccccccaacc ntnaattnan ttanccccn 660
ccccnggcc cggcctttta cnancntcnn nnacngggna aaaccnnngc ttncccaac 720
nnaatccnc t 731

```

<210> 20

<211> 754

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(754)

<223> n = A,T,C or G

<400> 20

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tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc 60
caacccccctc ntccaaatnn cnttttcgg gnggggggttc caaacccaan ttanntttgg 120
annttaaat aaatnttnt tggnggnna anccnaatgt nangaaagt naaccanta 180
tnancttnaa tncctggaaa ccngtngntt ccaaaaatnt ttaaccctta antccctcg 240
aaatngttna nggaaaaccc aanttctcnt aagggtgttt gaaggntnaa tnaaaanccc 300
nnccaattgt tttngccac gcctgaatta attgnttcc gntgttttcc nttaaaanaa 360
ggnnancccc ggttantnaa tccccccnnc cccaattata ccgantttt ttngaattgg 420
ganccncgg gaattaacgg ggnnnntccc tnttgggggg cnggnncccc cccntcggg 480
ggttngggnc aggnncnaat tgtttaaggg tccgaaaaat cctccnaga aaaaaanctc 540
ccaggntgag nntnggggtt ncccccccc canggccct ctcgnanagt tggggtttgg 600
ggggcctggg atttntttc cctnttnc tcccccccc ccnggganag aggttngngt 660
ttgntcnc ggccccnccn aaganccttn ccganttnan ttaaatccnt gcctnggcga 720
agtcnttgn agggntaaan ggccccctnn cggg 754

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<210> 21

<211> 755

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(755)

<223> n = A,T,C or G

<400> 21

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atcancccat gacccnaac nngggaccnc tcancggnc nnnnaccnc cggccnatca 60
nngtnagnnc actncnnttn natcacnccc cncnactac gcccnanc cnacgcncta 120
nncanattcc actganngcg cgangtngan ngagaaanct nataccanag ncaccanacn 180
ccagctgtcc nanaangcct nnnatacngg nnnatccaat ntgnancctc cnaagtattn 240
nncnnanatt gattttcctn anccgattac ccntncccc tanccctcc cccccacna 300
cgaaggcnct ggncnaagg nngcgnccnc cgctagntc cccncaagt cncncccta 360
aactcancn nattacncc ttcttgagta tcaactccc aatctcacc tactcaactc 420
aaaaanattn gatacaaat aatncaagcc tgnttatnac actntgactg ggtctctatt 480
ttagnngtcc ntnaancnt ctaatacttc cagtctncc tcnccaattt ccnaanggct 540
ctttcngaca gcatnttttg gtccccntt ggggtcttan ngaattgccc ttctnngaac 600

```

gggctentct	tttccctcgg	ttancctggn	ttcnnccggc	cagttattat	ttcccntttt	660
aaattcntnc	cntttanttt	tggcnttcna	aacccccggc	cttgaaaaacg	gccccctggt	720
aaaagggtgt	tttganaaaa	tttttgtttt	gttcc			755

<210> 22

<211> 849

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(849)

<223> n = A,T,C or G

<400> 22

tttttttttt	tttttangtg	tngtcgtgca	ggtagaggct	tactacaant	gtgaanacgt	60
acgctnggan	taangcgacc	cgantttctag	ganncnccct	aaaatcanac	tgtgaagatn	120
atcctgnnna	cgggaanggtc	accggnngat	nntgctaggg	tgncnctcc	cannncnttn	180
cataactcng	nggccctgcc	caccaccttc	ggcggcceng	ngnccggggc	cgggtcattn	240
gnnttaaccn	cactnngcna	ncggtttccn	nccccnneng	accnnggcca	tccgggggtnc	300
tctgtcttcc	cctgnagncn	anaaantggg	ccncggnccc	ctttaccct	nnacaagcca	360
cngcenteta	ncncncccc	cccctccant	nngggggact	gccnanngt	ccgttctng	420
nnaccccnnn	gggtncctcg	gttgctcgant	cnaccgnang	ccanggattc	cnaaggaagg	480
tgcgttnttg	gcccctaccc	ttcgctnccg	nncacccttc	ccgacnanga	nccgctccc	540
cncnncgnng	cctcncctcg	caacacccgc	nctentcngt	ncggnnnccc	ccccacccgc	600
nccctcncnc	ngncgnancn	ctcncncnc	gtctcannca	ccaccccgcc	ccgccaggcc	660
ntcanccacn	ggngacnng	nagcncntc	gcncgcgc	gcgncnccct	cgcncngaa	720
ctnctcngg	ccantnncgc	tcaancnna	cnaaacgcgc	ctgcgcggcc	cgnagcgncc	780
ncctcncga	gtcctcccgn	cttcnacc	angrnttccn	cgaggacacn	nnaccccgcc	840
nncangcgg						849

<210> 23

<211> 872

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(872)

<223> n = A,T,C or G

<400> 23

gcgcaaaacta	tacttcgtc	gnactcgtgc	gcctcgtcnc	tcttttccctc	cgcaaccatg	60
tctgacnanc	ccgattnggc	ngatatcnan	aagntcganc	agtccaaact	gantaacaca	120
cacacnncan	aganaaatcc	nctgccttcc	anagtanacn	attgaacnng	agaaccangc	180
nggcgaatcg	taatnaggcg	tgcgcgcgca	atntgtcnc	gtttattntn	ccagctcnc	240
ctnccnacc	tacntcttcn	nagctgtcnn	acccctngtn	cgnaccccc	naggctcgga	300
tccgggtttnn	nntgaccng	cnnccctcc	ccccctccat	nacgancnc	ccgcaccacc	360
nanngcncgc	nccccgnct	cttcgcnc	ctgtcctntn	ccccgtngc	ctggenengn	420
accgcattga	ccctcgccnn	ctncnngaaa	ncgnanacgt	ccgggttggn	annancgtg	480
tgggnnnngcg	tctgcncgc	gttccttcn	ncncttcca	ccatcttct	tacnggggtct	540
ccncgcctc	tcnnncacnc	cctgggaagc	tntcctntgc	cccccttnac	tccccctt	600
cgnctgncc	cgnccccacc	ntcatttnca	nacgntcttc	acaannncc	ggntnnctcc	660
cnancngncn	gtcanccnag	ggaagggngg	ggnnccnntg	nttgacgttg	nggngangtc	720
cgaanantcc	tcnccntcan	cnctaccct	cgggcgnnct	ctcngttnc	aacttancaa	780

ntctcccccg ngngcncttc tcagcctcnc ccccccnct ctctgcantg tncctctctc 840
tnaccnntac gantnttcgn cccccctttt cc 872

<210> 24
<211> 815
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (815)
<223> n = A,T,C or G

<400> 24
gcattgcaagc ttgagtattc tatagngtca cctaaatanc ttggcntaat catgggtcnta 60
nctgncttcc tgtgtcaaat gtatacnaa tanatatgaa tctnatntga caaganngtg 120
tctnncatta gtaacaantg tnnrtgtccat cctgtcngan canattccca tnnattncgn 180
cgcattcn cn cantatn taatngggaa ntcnnntnnn ncaccnncat ctatcntncc 240
gccccctgac tggagagat ggatnanttc tnnntngacc nacatgttca tcttggattn 300
aanaccccc cgcngnccac cggttngnng cnagccnntc ccaagacctc ctgtggaggt 360
aacctgcgtc aganncatca aacntgggaa acccgcnnc angtnnaagt ngnnncanan 420
gatcccgctc aggnntnacc atcccttcnc agcgcacct ttngtgcctt anagnnagc 480
gtgtccnanc cncatcaat ganacgcgcc agnccanccg caattnggca caatgtcgcnc 540
gaacccccca gggggantna tncaaanccc caggattgtc cncncangaa atcccnanc 600
ccnccctac cennctttgg gacngtgacc aantcccgga gtncaggtcc ggcngnctc 660
ccccaccggt nncntgggg ggtgaanct cngnntcanc cngncgaggn ntcgnaagga 720
accggnccn ggncgaanng ancnntcnga agngccnct cgtataaccc cccctcncca 780
nccnncngnt agntcccccc cngggtnccg aangg 815

<210> 25
<211> 775
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (775)
<223> n = A,T,C or G

<400> 25
ccgagatgtc tcgctccgtg gccttagctg tgcctgcgct actctctctt tctggcctgg 60
aggctatcca gcgtactcca aagattcagg tttactcacg tcatccagca gagaatggaa 120
agtcaaattt cctgaattgc tatgtgtctg ggtttcatcc atccgacatt gaanttgact 180
tactgaagaa tgganagaga attgaaaag tggagcatte agacttgtct ttcagcaagg 240
actggctctt ctatctctg tactacactg aattcacccc cactgaaaaa gatgagtatg 300
cctgccgtgt gaaccatgtg actttgtcac agcccaagat agttaagtgg gatcgagaca 360
tgtaagcagn cnnatggaa gtttgaagat gccgcatctg gattggatga attccaaatt 420
ctgcttgctt gcnttttaaat antgatatgc ntatacacce taccctttat gncccccatt 480
tgtaggggtt acatnantgt tcnctnngga catgatcttc ctttataant cncncttcg 540
aattgccgt cncnngttn ngaatgttcc cnaaaccacg gttggctccc ccaggtcncc 600
tcttacggaa gggcctgggc cnccttncaa ggttggggga accnaaaatt tcncttntgc 660
cncnccncca cnccttngg nncnctntt ggaaccttc cnattccctc tggcctcnna 720
nccttnncta anaaaacttn aaancgtngc naaannnttn acttcccccc ttacc 775

<210> 26

<211> 820
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(820)
 <223> n = A,T,C or G

<400> 26
 anattantac agtgtaatct ttteccagag gtgtgtanag ggaacggggc ctagaggcat 60
 cccanagata ncttatanca acagtgtctt gaccaagagc tgctgggcac atttcctgca 120
 gaaaagggtg cggtcccat cactcctcct ctcccatagc catcccagag gggtagtag 180
 ccatcangcc ttcggtggga gggagtcang gaaacaacan accacagagc anacagacca 240
 ntgatgacca tgggcgggag cgagcctctt ccctgnaccg gggtaggana nganagccta 300
 nctgaggggt cacactataa acgttaacga ccnagatnan cacctgtctc aagtgcaccc 360
 ttcctacctg acnaccagn accnnnaact gcngcctggg gacagcctg ggancagcta 420
 acnnagcact cacctgcccc cccatggcgc tncgctcctc tggctcctgnc aagggaagct 480
 ccctgttgga attncgggga naccaaggga nccccctcct ccactgtga aggaaaaann 540
 gatggaattt tnccttccg gccnntcccc tcttcttta cagccccct nntactctc 600
 tccctctntt ntcctgncnc acttttnacc ccnnnatttc ccttnattga tcggannctn 660
 ganattccac tnnccctnc cntcnatcng naanacnaaa nactntctna ccnnggggat 720
 gggnnccctc ntcactctct ctttttctct accnccnntt ctttgctct ccttngatca
 780tccaacntc gntggcctn cccccennn tcttttccc
 820

<210> 27
 <211> 818
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(818)
 <223> n = A,T,C or G

<400> 27
 tctgggtgat ggctcttcc tctcagggg cctctgactg ctctgggcca aagaatctct 60
 tgtttcttct ccgagcccca ggcagcgggtg attcagccct gcccaacctg attctgatga 120
 ctgcggatgc tgtgacggac ccaaggggca aatagggtcc caggggtccag ggaggggccc 180
 ctgctgagca ctccgcccc tcacctgcc cagccctgc catgagctct gggctgggtc 240
 tccgctcca gggttctgct ctccangca ngccancaaag tggcgtggg ccacactggc 300
 ttcttctgct ccctccctg gctctganc tctgtcttcc tgtcctgtgc angccttg 360
 gatctcagtt tccctcctc anngaactct gtttctgann tcttcantta actntgantt 420
 tatnaccnan tggnetgtnc tgtcnnactt taatgggcn gaccggctaa tccctccctc 480
 nctcccttcc anttcnnna accncttnc cntctctcc cntancccg ccngggaanc 540
 ctctttgcc ctnaccang gccnnnaccg ccctnnctn ggggggcnng gtnnctncnc 600
 ctgntnnccc cctcncnnt tncctcgtcc cnnncnccn nngcannttc ncngtcccn 660
 tnnctcttcn ngntcgnaa ngntcncntn tnnnnngncn ngntnntnnc tccctctcnc 720
 cnnntgnang tntttnnnnc ncngncccc nnnnnnnnn nggnntnnn tctncncngc 780
 cccnncccc ngnattaagg cctcnnctc ccggcnc 818

<210> 28
 <211> 731
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 28

aggaagggcg gagggatatt gtangggatt gagggatagg agnataangg gggaggtgtg	60
tccaacatg anggtgnngt tctcttttga angaggggtg ngtttttann ccnggtgggt	120
gattnaaccc cattgtatgg agnnaaagggn tttnagggat ttttcggctc ttatcagtat	180
ntanattcct gtnaatcgga aaatnatntt tcnnncggaa aatnttgctc ccatccgnaa	240
attnctcccg ggtagtgcac nttngggggg cngccangtt tcccaggctg ctanaatcgt	300
actaaagntt naagtgggan tncaaatgaa aacctnncac agagnatccn tacccgactg	360
tnnnttnccct tcgcccctntg actctgcngg agcccaatac ccnngngnat gtcncccn	420
nnngcgnenc tgaaannnnc tcngggctnn gancatcang gggtttcgca tcaaaagcnn	480
cgtttcncat naaggcactt tngcctcacc caaccnctng ccctcncca tttngccgctc	540
nggttcnccct acgctnnctg cncctnnntn ganattttnc ccgcctnggg naancctcct	600
gnaatgggta gggnccttntc ttttnaccnn gnggtntact aatcnctnc acgctnctt	660
tctcnacccc ccccctttt caatcccanc ggcnaatggg gtctcccn cgangggggg	720
nnccccann c	731

<210> 29

<211> 822

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(822)

<223> n = A,T,C or G

<400> 29

actagtccag tgtgggtggaa ttccattgtg ttgggggncnc ttctatgant antnttagat	60
cgetcanacc tcacancctc ccnacnangc ctataangaa nannaataga nctgtncnnt	120
atntntacnc tcatanncct cnnnaccac tccctcttaa cccntactgt gcctatngcn	180
tnnctantct ntgcgcctn cnanccaccn gtgggcnac cncnngnatt ctcnatctcc	240
tncccatn tn gcctananta ngtncatacc ctatactac nccaatgcta nnnctaancn	300
tccatnantt annntaacta ccactgacnt ngactttcnc atnanctcct aatttgaatc	360
tactctgact cccacngcct annnattagc ancntcccc nacnatntct caaccaaatc	420
ntcaacaacc tatctantctg ttcnccaacc nttncctccg atccccnnac aacccccctc	480
ccaaataccc nccacctgac ncctaaccn caccatccc gcaagccnan ggcatttan	540
ccactggaat cacnatngga naaaaaaac ccnaactctc tancncnnat ctccctaana	600
aatnctcctn naatttactn ncantnccat caancccaen tgaaacnnaa cccctgtttt	660
tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc cccccnctnc	720
ccnaatgaag gncncccaat cnangaaacg nccntgaaaa ancnaaggcna anannntccg	780
canatcctat cccttanttn ggggnccctt nccngggcc cc	822

<210> 30

<211> 787

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(787)

<223> n = A,T,C or G

<400> 30

cggccgcctg	ctctggcaca	tgcctcctga	atggcatcaa	aagtgatgga	ctgcccattg	60
ctagagaaga	ccttctctcc	tactgtcatt	atggagccct	gcagactgag	ggctcccctt	120
gtctgcagga	tttgatgtct	gaagtcgtgg	agtgtggctt	ggagctcctc	atctacatna	180
gctggaagcc	ctggagggcc	tctctcgcca	gcctccccct	tctctccacg	ctctccangg	240
acaccagggg	ctccaggcag	cccattatct	ccagnangac	atgggtgttc	tccacgcgga	300
cccatggggc	ctgnaaggcc	agggctctct	ttgacaccat	ctctcccgtc	ctgcctggca	360
ggccgtggga	tccactantt	ctanaacggn	cgccaccncg	gtgggagctc	cagcttttgt	420
tcccnttaat	gaaggttaat	tgcncgcttg	gcgtaatcat	nggtcanaac	tntttcctgt	480
gtgaaattgt	ttntccccct	ncnattccnc	ncnacatacn	aacccggaan	cataaagtgt	540
taaagcctgg	gggtngcctn	nngaataaac	tnaactcaat	taattgcgtt	ggctcatggc	600
ccgctttccn	ttcnggaaaa	ctgtctntccc	ctgcnttntt	gaatcggccca	ccccccnggg	660
aaaagcgggt	tgcnttttng	ggggntcctt	ccncttcccc	cctcncctaan	ccctnccgct	720
cggtcgttnc	nggtngcggg	gaangggnat	nnnctccnc	naagggggng	agnnngntat	780
ccccaaa						787

<210> 31

<211> 799

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(799)

<223> n = A,T,C or G

<400> 31

tttttttttt	tttttttggc	gatgctactg	tttaattgca	ggaggtgggg	gtgtgtgtac	60
catgtaccag	ggctattaga	agcaagaagg	aaggaggagg	ggcagagcgc	cctgctgagc	120
aacaaaggac	tcctgcagcc	ttctctgtct	gtctcttggc	gcaggcacat	ggggaggcct	180
cccgagggtg	ggggggccacc	agtccagggg	tgggagcact	acanggggtg	ggagtgggtg	240
gtggctggtn	cnaatggcct	gncacanatc	cctacgattc	ttgacacctg	gatttcacca	300
ggggaccttc	tgttctccca	nggnaacttc	ntnnatctcn	aaagaacaca	actgtttctt	360
cngcanttct	ggctgttcat	ggaaagcaca	ggtgtccnat	ttnggctggg	acttggtaca	420
tatggttccg	gcccacctct	ccntcnaaan	aagtaattca	ccccccccc	ccntctnttg	480
cctgggcccct	taantaccca	caccggaact	canttantta	ttcatcttng	gntgggcttg	540
ntnatcnccn	cctgaangcg	ccaagttgaa	aggccacgcc	gtncnccnctc	cccatagnan	600
nttttnncnt	canctaatgc	ccccccnggc	aacnatccaa	tccccccccc	tggggggccc	660
agcccanggc	ccccgnctcg	ggnnnccngn	cncgnantcc	ccaggntctc	ccantcngnc	720
ccnnngcncc	ccgcacgca	gaacanaagg	ntngagccnc	cgcannnnnn	nggtnnncnac	780
ctgccccccc	ccnnccgngg					799

<210> 32

<211> 789

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(789)

<223> n = A,T,C or G

<400> 32

tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
tttttncnag	ggcagggttta	ttgacaacct	cncgggacac	aancaggctg	gggacaggac	120
ggcaacaggc	tccggcgggc	gcggcgggcg	ccctacctgc	ggtaccaa	ntgcagcctc	180
cgctcccgt	tgatnttct	ctgcagctgc	aggatgccnt	aaaacagggc	ctcgccntn	240
ggtgggcacc	ctgggatttn	aatttccacg	ggcacaatgc	ggtcgcancc	cctcaccacc	300
nattaggaat	agtggtnnta	cccncnccg	ttggcncact	ccccntggaa	accacttntc	360
gcggctccgg	catctggtct	taaaccttgc	aaacnctggg	gccctctttt	tggttantnt	420
nccngccaca	atcatnactc	agactggcnc	gggctggccc	caaaaaan	ccccaaaa	480
ggncatgtc	ttnncgggt	tgctgcnatn	tncatcacct	cccgggcnca	ncaggncaac	540
ccaaaagttc	ttgnngcccn	caaaaaanct	ccggggggnc	ccagtttcaa	caaagtcac	600
ccccctggcc	cccaaactct	ccccccgntt	nctgggtttg	ggaaccacg	cctctnnctt	660
tggnnggcaa	gntggntccc	ccttcggggc	ccgggtgggc	ccnnctctaa	ngaaaaacnc	720
ntcctnnnca	ccatcccccc	nngnnacgnc	tancaangna	tccctttttt	tanaaacggg	780
ccccccnccg						789

<210> 33

<211> 793

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(793)

<223> n = A,T,C or G

<400> 33

gacagaacat	gttggatggt	ggagcacctt	tctatacgac	ttacaggaca	gcagatgggg	60
aattcatggc	tgttggagca	atanaacccc	agttctacga	gctgctgac	aaaggacttg	120
gactaaagtc	tgatgaactt	cccaatcaga	tgagcatgga	tgattggcca	gaaatgaana	180
agaagtttgc	agatgtat	gcaaagaaga	cgaaggcaga	gtggtgtcaa	atctttgacg	240
gcacagatgc	ctgtgtgact	ccggtttctga	cttttgagga	ggttggtcat	catgatcaca	300
acaangaacg	gggctcgttt	atcaccantg	aggagcagga	cgtgagcccc	cgcctgcac	360
ctctgctgtt	aaacacccca	gccatccctt	ctttcaaaag	ggatccacta	cttctagagc	420
ggncgccacc	gcggtggagc	tccagctttt	gttcccttta	gtgagggtta	attgcgcgct	480
tggcgtaatc	atggtcatan	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	540
acaacatacg	anccggaagc	atnaaat	aaagcctgg	ggtngcctaa	tgantgaact	600
nactcacatt	aattggcttt	gcgctcactg	cccgttttcc	agtcgggaaa	acctgtcctt	660
gccagctgcc	nttaataaat	cnggccaccc	cccggggaaa	aggcngtttg	cttnttgggg	720
cgcnccttccc	gctttctcgc	ttcctgaant	ccttcccccc	ggtctttcgg	cttgcggcna	780
acggtatcna	cct					793

<210> 34

<211> 756

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(756)

<223> n = A,T,C or G

<400> 34

ggcgcgaccg	gcatgtacga	gcaactcaag	ggcgagtggg	accgtaaaag	ccccaatctt	60
ancaagtgcg	gggaanagct	gggtcgactc	aagctagt	ttctggagct	caacttcttg	120

ccaaccacag	ggaccaagct	gaccaaacag	cagctaattc	tggcccgtga	catactggag	180
atcggggccc	aatggagcat	cctacgcaan	gacatcccct	ccttcgagcg	ctacatggcc	240
cagctcaaat	gctactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttctctg	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgcccaanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtcctgga	gcaatactga	tgganggcag	ctaccncaaa	gtnttcctgg	ccnagggtaa	480
catccccgc	cgagagctac	accttcttca	ttgacatcct	gctcgacact	atcagggatg	540
aaaatcgcn	ggttgctcca	gaaaggctnc	aanaanatcc	ttttcnctga	aggcccccg	600
atncnctagt	nctagaatcg	gcccgccatc	gcggtgganc	ctccaacctt	tcgttncctt	660
ttactgaggg	tttattggcg	cccttggcgt	tatcatggtc	acnccngtn	cctgtgttga	720
aattnttaac	cccccaaat	tccacgccna	cattnng			756

<210> 35

<211> 834

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (834)

<223> n = A,T,C or G

<400> 35

ggggatctct	anactnacct	gnatgcattg	ttgtcgggtg	ggtcgctgtc	gatgaanatg	60
aacaggatct	tgcccttgaa	gctctcggct	gctgtnttta	agttgctcag	tctgccgtca	120
tagtcagaca	cncctcttgg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttcngg	gctgtctgct	cggtgaactc	gatgacnang	ggcagctggg	tgtgtntgat	240
aaantccanc	angttctcct	tggtgacctc	cccttcaaag	ttgttcgggc	cttcatcaaa	300
cttctnnaan	angannancc	canctttgtc	gagctggnat	ttgganaaca	cgtcaccgtt	360
ggaaactgat	cccaaattgg	atgtcatcca	tcgcctctgc	tgccctgcaa	aaacttgctt	420
ggcncaaact	cgactcccn	tccttgaaag	aagccnatca	cacccccctc	cctggactcc	480
nncaangact	ctncegctnc	cccntccnng	cagggttggt	ggcannccgg	gccntgctc	540
ttcttcagcc	agttcacnat	nttcatcagc	ccctctgcca	gctgttntat	tccttggggg	600
ggaanccgtc	ttctcccttc	tgaannaact	ttgaccgtng	gaatagccgc	gcntcnccnt	660
acntnctggg	ccgggttcaa	antccctccn	ttgncnntcn	cctcgggcca	ttctggattt	720
nccnaacttt	ttcttctccc	cncctccnng	ngtttggntt	tttcatnggg	ccccaaactc	780
gctnttggtc	antccctctg	gggcntntan	cncctccnt	ggtcctntng	ggcc	834

<210> 36

<211> 814

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (814)

<223> n = A,T,C or G

<400> 36

cggncgcttt	ccngccgcgc	cccgtttcca	tgacnaaggc	tcccttcang	ttaaatacnn	60
cctagnaaac	attaatgggt	tgctctacta	atacatcata	cnaaccagta	agcctgcccc	120
naacgccaac	tcaggccatt	cctaccaaag	gaagaaaggc	tggtctctcc	acccccctgt	180
ggaaaggcct	gccttgtaag	acaccacaat	ncggctgaat	ctnaagtctt	gtgttttact	240
aatggaaaaa	aaaaataaac	aanagggttt	gttctcatgg	ctgcccaccg	cagcctggca	300
ctaaaacanc	ccagcgctca	cttctgcttg	ganaaatatt	ctttgctctt	ttggacatca	360

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ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttcccc catntttgtc      420
antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc      480
aggggagtc ntttncagtg gatctgccaa anantaccen tatcatcnnt gaataaaaag      540
gccccgaac ganatgcttc cancanctt taagacccat aatcctngaa ccatgggtgcc      600
cttccggtct gatccnaaag gaatgttctt ggggtccant ccctcctttg ttnccttacgt      660
tgntttggac cctgtctnng atnaccnaan tganatcccc ngaagcacc tncctctggc      720
atttganttt cntaaattct ctgccctaen nctgaaagca cnattccctn ggcncnaaan      780
ggngaactca agaaggtctn ngaaaaacca cncn                                     814

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<210> 37

<211> 760

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(760)

<223> n = A,T,C or G

<400> 37

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gcctgtgctt ctctctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg      60
gcgcagtgtt cgctgaaggg gttgtagtac cagcgcgagg tgctctcctt gcagagtcct      120
gtgtctggca ggtccacgca atgccctttg tctactggga aatggatgag ctggagctcg      180
tcnaanccac tcgtgtatct ttcacangca gcctctcccg aagcctcccg gcagttgggg      240
gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt      300
gggctgacag gtgccagaac acactggatn ggcctttcca tggaaaggcc tgggggaaat      360
cncctnancc caaactgcct ctcaaaggcc accttgacac ccccgacagg ctgaaatgc      420
actcttcttc ccaaaggtag ttgttcttgt tgcccaagca ncctccanca aacccaaanc      480
ttgcaaaatc tgctcctggg gggtcatnnn taccanggtt ggggaaanaa acccggcngn      540
ganccncttt gtttgaatgc naaggnaata atcctcctgt ctgtgctggg tggaaagca      600
caattgaact gttaacnttg ggccgngttc cncctnggtg gtctgaaact aatcacgctc      660
actggaaaaa ggtangtgcc ttccttgaat tcccaantt cccctngntt tgggtntttt      720
ctcctctncc ctaaaaatcg tnttcccccc cntangggc                                     760

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<210> 38

<211> 724

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(724)

<223> n = A,T,C or G

<400> 38

```

tttttttttt tttttttttt tttttttttt tttttaaaaa cccctcccat tgaatgaaaa      60
cttcnaaat tgccaaccc cctcnccaa atnccattt cggggggggg gttccaaacc      120
caaattaat ttgganttta aattaaatnt tnatnngggg aanaanccaa atgtnaagaa      180
aatttaaccc attatnaact taaatnccn gaaaccntg gnttccaaaa atttttaacc      240
cttaaatccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaaggtt      300
ngatttaaac ccccttnant tnttttnacc cnnngctnaa ntatttngnt tccggtgttt      360
tcctnttaan cntnggtaac tcccngtaat gaannnccct aanccaatta aaccgaattt      420
tttttgaatt ggaaattccn ngggaattna cgggggtttt tcccttttgg gggccatncc      480
ccncttttgc ggggttgggn ntagggtgaa ttttttnang ncccaaaaaa ncccccaana      540
aaaaaactcc caagnnttaa ttngaantnc ccccttccca ggccttttgg gaaaggnggg      600

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tttntggggg	ccngggantt	cnttccccc	ttncncccc	ccccccnggt	aaanggttat	660
ngnntttggt	ttttgggccc	cttnanggac	cttccggatn	gaaattaaat	ccccgggncg	720
gccg						724

<210> 39

<211> 751

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(751)

<223> n = A,T,C or G

<400> 39

tttttttttt	tttttctttg	ctcacattta	atttttat	tgattttttt	taatgctgca	60
caacacaata	tttatctcat	ttgtttcttt	tatttcattt	tatttgtttg	ctgctgctgt	120
tttatcttatt	tttactgaaa	gtgagaggga	acttttggtg	ccttttttcc	tttttctgta	180
ggccgcctta	agctttctaa	atttggaa	tctaagcaag	ctgaanggaa	aaggggggtt	240
cgcaaatca	ctcgggggaa	nggaaagggt	gctttgttaa	tcatgcccta	tggtgggtga	300
ttaactgctt	gtacaattac	ntttcacttt	taattaattg	tgctnaangc	tttaattana	360
cttggggggt	ccctccccc	accaacccc	ctgacaaaa	gtgccngccc	tcaaatnatg	420
tcccgcnnt	cnttgaaaca	cacngcngaa	ngttctcatt	ntcccccnc	caggtnaaaa	480
tgaagggtta	ccatntttta	cncacctcc	acntggcnnn	gcctgaatcc	tcnaaaan	540
ccctcaancn	aattnctnng	ccccggtcnc	gcntnnngtc	cncgggggt	ccgggaantn	600
cacccccnga	anncnntnnc	naacnaaatt	ccgaaaatat	tcccnntcnc	tcaattcccc	660
cnnagactnt	cctcnncnan	cnaatttttc	ttttntcac	gaacncgnnc	cnnaaatgn	720
nnnncnctc	cnctngtcn	naatcnccan	c			751

<210> 40

<211> 753

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(753)

<223> n = A,T,C or G

<400> 40

gtggattttt	ctgtaagatc	aggtgttctt	ccctcgtagg	tttagaggaa	acaccctcat	60
agatgaaaac	ccccccgaga	cagcagcact	gcaactgcca	agcagccggg	gtaggagggg	120
cgccctatgc	acagctgggc	ccttgagaca	gcagggcttc	gatgtcaggc	tcgatgtcaa	180
tggtctggaa	gcggcggtg	tacctgcgta	ggggcacacc	gtcagggccc	accaggaact	240
tctcaaagtt	ccaggcaacn	tcgttgcgac	acaccggaga	ccagggtgatn	agcttgggggt	300
cggtcataan	cgcggtggcg	tcgtcgctgg	gagctggcag	ggcctccgc	aggaaggcna	360
ataaaagggtg	cgcccccgca	ccgttcant	cgcacttctc	naanaccatg	angttgggct	420
cnaaccacc	accannccgg	acttccttga	nggaattccc	aaatctcttc	gntcttgggc	480
ttctnctgat	gccctanctg	gttgcccn	atgccaanca	nccccaancc	ccggggtcct	540
aaanccccc	cctcctcntt	tcatctgggt	tntntcccc	ggacntgggt	tcctctcaag	600
ggancccata	tctcnaccan	tactcacnt	nccccccnt	gnnaccanc	cttctanngn	660
ttccncccc	ncctctggcc	cntcaaan	gcttnacna	cctgggtctg	ccttcccccc	720
tncctatct	gnaccccn	ttgtctcan	tnt			753

<210> 41

<211> 341
 <212> DNA
 <213> Homo sapien

<400> 41
 actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaagt 60
 agtgaaccca tccttgattt atatacatat atgttctcag tattttggga gcctttccac 120
 ttctttaaac ctgttcatt atgaacactg aaaataggaa tttgtgaaga gttaaaaagt 180
 tatagcttgt ttacgtagta agtttttgaa gtctacattc aatccagaca cttagttgag 240
 tgttaaactg tgatttttaa aaaatatcat ttgagaatat tctttcagag gtattttcat 300
 ttttactttt tgattaattg tgttttatat attagggtag t 341

<210> 42
 <211> 101
 <212> DNA
 <213> Homo sapien

<400> 42
 acttactgaa tttagttctg tgctcttctt tatttagtgt tgtatcataa atactttgat 60
 gtttcaaaca ttctaaataa ataattttca gtggcttcat a 101

<210> 43
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 43
 acatctttgt tacagtctaa gatgtgttct taaatcacca ttccttctctg gtcctcacc 60
 tccagggtgg tctcacactg taattagagc tattgaggag tctttacagc aaattaagat 120
 tcagatgcct tgctaagtct agagttctag agttatgtt cagaaagtct aagaaacca 180
 cctcttgaga ggtcagtaaa gaggacttaa tatttcatat ctacaaaatg accacaggat 240
 tggatacaga acgagagtta tcctggataa ctacagagctg agtacctgcc cgggggccgc 300
 tcgaa 305

<210> 44
 <211> 852
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(852)
 <223> n = A,T,C or G

<400> 44
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 gattatttgg tgtgtgtttt gggttgtgtc caaagtattg gcagcttcag ttttcatttt 120
 ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct 180
 ccagaatttc tctttttag taatatctca tagctcggct gagcttttca taggtcatgc 240
 tgctgttgtt cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga 300
 agacgccctc agatcggctt tccattttta ttaatcctgg gttcttgtct gggttcaaga 360
 ggatgtcgcg gatgaattcc cataagttag tccctctcgg gttgtgcttt ttggtgtggc 420
 acttggcagg ggggtcttgc tcttttttca tatcagggtga ctctgcaaca ggaaggtgac 480
 tgggtgttgt catggagatc tgagcccgcc agaaagtgtt gctgtccaac aaatctactg 540
 tgctaccata gttggtgtca tataaatagt tctngtcttt ccagggtgtc atgatggaag 600

gctcagtttg	ttcagtccttg	acaatgacat	tgtgtgtgga	ctggaacagg	tcactactgc	660
actggccggt	ccacttcaga	tgctgcaagt	tgctgtagag	gagntgcccc	gccgtccctg	720
ccgcccgggt	gaactcctgc	aaactcatgc	tgcaaagggtg	ctcgccgttg	atgtcgaact	780
cntggaaagg	gatacaattg	gcatccagct	ggttggtgtc	caggagggtga	tggagccact	840
cccacacctg	gt					852

<210> 45

<211> 234

<212> DNA

<213> Homo sapien

<400> 45

acaacagacc	cttgctcgct	aacgacctca	tgctcatcaa	gttggacgaa	tccgtgtccg	60
agtctgacac	catccggagc	atcagcattg	cttcgcagtg	ccctaccgcg	gggaactctt	120
gcctcgtttc	tggctgggggt	ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	180
tgaacgtgtc	ggtggtgtct	gaggaggtct	gcagtaagct	ctatgaccgc	ctgt	234

<210> 46

<211> 590

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (590)

<223> n = A,T,C or G

<400> 46

actttttatt	taaatgttta	taaggcagat	ctatgagaat	gatagaaaac	atggtgtgta	60
atttgatagc	aatatttttg	agattacaga	gttttagtaa	ttaccaatta	cacagttaaa	120
aagaagataa	tatattccaa	gcanatacaa	aatatcta	gaaagatcaa	ggcaggaaaa	180
tgantataac	taattgacaa	tggaaaatca	attttaatgt	gaattgcaca	ttatccttta	240
aaagctttca	aaanaanaa	ttattgcagt	ctanttaatt	caaacagtgt	taaatgggtat	300
caggataaan	aactgaagg	canaaagaat	taattttcac	ttcatgtaac	ncacccanat	360
ttacaatggc	ttaaattgcan	ggaaaaagca	gtggaagtag	ggaagtantc	aaggtctttc	420
tggctctctaa	tctgccttac	tctttgggtg	tggctttgat	cctctggaga	cagctgccag	480
ggctcctgtt	atatccacaa	tcccagcagc	aagatgaagg	gatgaaaaag	gacacatgct	540
gccttccttt	gaggagactt	catctcactg	gccaacactc	agtcacatgt		590

<210> 47

<211> 774

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (774)

<223> n = A,T,C or G

<400> 47

acaagggggc	ataatgaagg	agtggggana	gatttttaaag	aaggaaaaaa	aacgaggccc	60
tgaacagaat	tttcctgnac	aacggggctt	caaaaataatt	ttcttgggga	ggttcaagac	120
gcttcactgc	ttgaaactta	aatggatgtg	ggacanaatt	ttctgtaatg	accctgaggg	180
cattacagac	gggactctgg	gaggaaggat	aaacagaaaag	gggacaaaag	ctaattccaa	240
aacatcaaag	aaaggaaggt	ggcgtcatac	ctcccagcct	acacagttct	ccagggtctc	300

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cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctctgtgtg      360
ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgctgat cctgcgtggc      420
ccacactcct tgaacacaca tccccagggt atattcctgg acatggctga acctcctatt      480
cctacttccg agatgccttg ctccctgcag cctgtcaaaa tccactcac cctccaaacc      540
acggcatggg aagcctttct gacttgcttg attactccag catcttggaa caatccctga      600
ttccccactc cttagaggca agataggggt gttaagagta gggctggacc acttggagcc      660
aggctgctgg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct      720
tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt          774

    <210> 48
    <211> 124
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(124)
    <223> n = A,T,C or G

    <400> 48
canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt      60
ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact      120
tggt                                              124

    <210> 49
    <211> 147
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(147)
    <223> n = A,T,C or G

    <400> 49
gccgatgcta ctattttatt gcaggagggt ggggtgtttt tattattctc tcaacagctt      60
tgtggctaca ggtgggtgtc gactgcatna aaaanttttt tacgggtgat tgcaaaaatt      120
ttagggcacc catatcccaa gcantgt                      147

    <210> 50
    <211> 107
    <212> DNA
    <213> Homo sapien

    <400> 50
acattaaatt aataaaaagga ctgttgggggt tctgctaaaa cacatggctt gatatatattgc      60
atggtttgag gttaggagga gttaggcata tgttttggga gaggggt                      107

    <210> 51
    <211> 204
    <212> DNA
    <213> Homo sapien

    <400> 51
gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgcacgg      60

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cggaaggaa aggcagagaa gtgacaccgt caggggggaaa tgacagaaag gaaaatcaag 120
gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttgGCCA 180
ctccctttt gggaccagca atgt 204

<210> 52

<211> 491

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(491)

<223> n = A,T,C or G

<400> 52

acaaagataa catTTatctt ataacaaaaa tttgatagtt ttaaagggtta gtattgtgta 60
gggtattttt caaaagacta aagagataac tcagggtaaaa agttagaaat gtataaaaca 120
ccatcagaca ggTTTTTaaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa 180
aaaacttctt gtatcaattt cttttgttca aaatgactga ctttaantatt tttaaatatt 240
tcanaaacac ttcctcaaaa attttcaana tggtagcttt canatgtnc ctcagtccca 300
atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc 360
atgcaacagt gtcttttctt tncTTTTtct tttttttttt ttacaggcac agaaactcat 420
caattttatt tggataacaa agggctctca aatttatattg aaaaataaat ccaagttaat 480
atcactcttg t 491

<210> 53

<211> 484

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(484)

<223> n = A,T,C or G

<400> 53

acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga 60
gtattaacag ttgctgaagt ttgggtatttt tatgcagcat tttctttttg ctttgataac 120
actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct 180
caatcaaadc tctacataac actatagtaa ttaaaacggt aaaaaaaagt gtgaaatct 240
gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc 300
agctttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttggt gcctctccct 360
aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncg 420
tancttgant ctgtgtattc caggancagg cggatggaat gggccagccc ncggatgttc 480
cant 484

<210> 54

<211> 151

<212> DNA

<213> Homo sapien

<400> 54

actaaacctc gtgcttgtga actccatata gaaaacgggt ccatccctga acacggctgg 60
ccactgggta tactgctgac aaccgcaaca acaaaaaacac aaatccttgg cactggctag 120
tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55
<211> 91
<212> DNA
<213> Homo sapien

<400> 55
acctggcttg tctccgggtg gttcccggcg cccccacgg tccccagaac ggacactttc 60
gcctccagt ggatactcga gccaaagtgg t 91

<210> 56
<211> 133
<212> DNA
<213> Homo sapien

<400> 56
ggcggatgtg cgttggttat atacaaatat gtcattttat gtaagggact tgagtatact 60
tggatttttg gtatctgtgg gttgggggga cgggccagga accaatacc catggatacc 120
aagggacaac tgt 133

<210> 57
<211> 147
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(147)
<223> n = A,T,C or G

<400> 57
actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60
gactgggagc tgagcccttc ctttgcgcc tgcctcagag gattgttgcc gacntgcana 120
tctcantggg ctggatncat gcagggt 147

<210> 58
<211> 198
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(198)
<223> n = A,T,C or G

<400> 58
acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60
tgattacata catttatcct ttaaaaaaga tgtaaatctt aatttttatg ccatctatta 120
attaccaat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180
ttgacttcta agtttgg 198

<210> 59
<211> 330
<212> DNA
<213> Homo sapien

<400> 59
 acaacaaatg gggttgagg aagtcttata agcaaaactg gtgatggcta ctgaaaagat 60
 ccattgaaaa ttatcattaa tgattttaaa tgacaagtta tcaaaaactc actcaatttt 120
 cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa 180
 tacagtcaat aaatgacaaa gccagggcct acagggtggt tccagacttt ccagaccag 240
 cagaaggaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt 300
 tttcgtcttt attggacttc tttgaagagt 330

<210> 60
 <211> 175
 <212> DNA
 <213> Homo sapien

<400> 60
 accgtgggtg ccttctacat tcctgacggc tccttcacca acatctggtt ctacttcggc 60
 gtcgtgggct ccttcctctt catcctcacc cagctgggtg tgctcatcga ctttgcgcac 120
 tcctggaacc agcgggtggc gggcaaggcc gaggagtgcg attcccgtgc ctggt 175

<210> 61
 <211> 154
 <212> DNA
 <213> Homo sapien

<400> 61
 accccacttt tcctcctgtg agcagtctgg acttctcact gctacatgat gagggtgagt 60
 gggtgttgct cttcaacagt atcctcccct ttccggatct gctgagccgg acagcagtgc 120
 tggactgcac agccccgggg ctccacattg ctgt 154

<210> 62
 <211> 30
 <212> DNA
 <213> Homo sapien

<400> 62
 cgctcgagcc ctatagtgag tcgtattaga 30

<210> 63
 <211> 89
 <212> DNA
 <213> Homo sapien

<400> 63
 acaagtcatt tcagcacctt ttgctcttca aaactgacca tcttttatat ttaatgcttc 60
 ctgtatgaat aaaaatggtt atgtcaagt 89

<210> 64
 <211> 97
 <212> DNA
 <213> Homo sapien

<400> 64
 accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa gggtctgcag 60
 aatcagtgca tccaggattg gtccttgat ctggggg 97

<210> 65
 <211> 377
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(377)
 <223> n = A,T,C or G

<400> 65
 acaacaanaa ntcccttctt taggccactg atggaaacct ggaacccctt tttgatggca 60
 gcatggcgct ctaggccttg acacagcggc tgggggtttg gctntcccaa accgcacacc 120
 ccaaccctgg tctacccaca nttctggcta tgggctgtct ctgccactga acatcagggt 180
 tcggtcataa natgaaatcc caanggggac agagggtcagt agaggaagct caatgagaaa 240
 ggtgctgttt gctcagccag aaacagctg cctggcattc gccgctgaac tatgaacccg 300
 tgggggtgaa ctaccccan gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360
 gggcgggagg agcatgt 377

<210> 66
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 66
 acgcctttcc ctcagaattc agggaagaga ctgtcgctg ccttcctcctg ttgttgctg 60
 agaaccctgt tgcccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120
 aggaactaac tgcaccctgg tctctcccc agtccccagt tcaccctcca tccctcacct 180
 tctccactc taagggatat caacactgcc cagcacaggg gccttgaatt tatgtggttt 240
 ttatatattt ttttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300
 tgttt 305

<210> 67
 <211> 385
 <212> DNA
 <213> Homo sapien

<400> 67
 actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60
 ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcaggt ctgagagttc 120
 cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180
 tgtgctgtgc tggagattca cttttgagag agttctcctc tgagacctga tctttagagg 240
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300
 cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac 360
 catagtttct gtgctagtgg accgt 385

<210> 68
 <211> 73
 <212> DNA
 <213> Homo sapien

<400> 68
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60
 gtttttttaa tgg 73

<210> 69
 <211> 536
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(536)
 <223> n = A,T,C or G

<400> 69
 actagtccag tgtggtggaa ttccattgtg ttgggggctc tcaccctcct ctccctgcagc 60
 tccagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120
 cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180
 cccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240
 cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgcgggt 300
 actaagagcc aggaacaga ccgttggggg ggtgaattac ttcttcgacg tagaggtggg 360
 ccgaaccata tgtaccaagt ccagcccaa cttggacacc tgtgccttcc atgaacagcc 420
 agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagttccct ggggagaaca 480
 gaangtcctt gggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70
 <211> 477
 <212> DNA
 <213> Homo sapien

<400> 70
 atgaccctta acaggggccc tctcagccct cctaatagacc tccggcctag ccatgtgatt 60
 tcacttccac tccataacgc tcttcatact aggcctacta accaacacac taaccatata 120
 ccaatgatgg cgcgatgtaa cagagaaaag cacataccaa ggccaccaca caccacctgt 180
 ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagttt ttttcttcgc 240
 agggattttt ctgagccttt taccactcca gcctagcccc taccctccaa ctaggagggc 300
 actggccccc aacaggcatc accccgctaa atcccctaga agtcccactc ctaaacacat 360
 ccgtattact cgcatacagga gtatcaatca cctgagctca ccatagtcta atagaaaaca 420
 accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctatcttt 477

<210> 71
 <211> 533
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(533)
 <223> n = A,T,C or G

<400> 71
 agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact 60
 aggtattaat agatatgtaa agaaagaaat cacaccatta ataatggtaa gattggttta 120
 tgtgatttta gtggatattt tggcaccctt atatatgttt tccaaacttt cagcagtgat 180
 attattttcca taacttaaaa agtgagtgtt aaaaagaaaa tctccagcaa gcatctcatt 240
 taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttta aaaagctgtc 300
 aaatagggtg gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360
 agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg 420
 cttcgttaatt ttggagtang aggttccctc ctcaattttg tatttttaaa aagtacatgg 480
 taaaaaaaaa aattcacaac agtatataag gctgtaaaaat gaagaattct gcc 533

<210> 72
 <211> 511
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(511)
 <223> n = A,T,C or G

<400> 72
 tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta 60
 aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa 120
 aagccgcagg atgtctacac tatancaggc gctatttggg ttggctggag gagctgtgga 180
 aaacatggan agattggtgc tgganacgc cgtggctatt cctcattgtt attacanagt 240
 gaggttctct gtgtgccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300
 cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac 360
 gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgcccc gtctgttatg 420
 atttctctcc attgcagcna naaaccggtt cttctaagca aacncagggtg atgatggcna 480
 aaatacaccc cctcttgaag naccnggagg a 511

<210> 73
 <211> 499
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(499)
 <223> n = A,T,C or G

<400> 73
 cagtgccagc actggtgccca gtaccagtac caataacagt gccagtgccca gtgccagcac 60
 cagtgggtggc ttcagtgtctg gtgccagcct gaccgccact ctcacatttg ggctcttgcg 120
 tggccttggg ggagctgggt ccagcaccag tggcagctct ggtgcctgtg gtttctccta 180
 caagtggat tttagatatt gttaatcttg ccagtcttct tcttcaagcc aggggtgcac 240
 ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagtggaca 300
 ctctgcatta aatctatttg ccatttctga aaaaaaaaaa aaaaaaaggg cggccgctcg 360
 antctagagg gcccgtttta acccgctgat cagcctcgac tgtgccttct anttgccagc 420
 catctgttgt ttgcccctcc cccgntgcct tccttgaccc tggaaagtgc cactcccact 480
 gtcctttcct aantaaat 499

<210> 74
 <211> 537
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(537)
 <223> n = A,T,C or G

<400> 74
 tttcatagga gaacacactg aggagatact tgaagaattt ggattcagcc gcgaagagat 60

```

ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctctaact 120
tccaggccca cggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa 180
cattgtatgc atggaaacat ggaggaacag tattacagtg tcctaccact ctaatcaaga 240
aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag 300
ggcttttgat ttataanact ttgggtactt atactaaatt atggtagtta tactgccttc 360
cagtttgctt gatataattg ttgatattaa gattcttgac ttatatattg aatgggttct 420
actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat 480
tctacaatgt agaaaatgaa ggaaatgccc caaattgtat ggtgataaaa gtcccgct 537

```

<210> 75

<211> 467

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(467)

<223> n = A,T,C or G

<400> 75

```

caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60
tgcattattac acgtacctcc tcctgctcct caagtagtgt ggtctatttt gccatcatca 120
cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180
tggcacaagg aggccatctt ttctcatcgc gttattgtcc ctagaagcgt cttctgagga 240
tctagttggg ctttctttct gggtttgggc catttcantt ctcatgtgtg tactattcta 300
tcattattgt ataacgggtt tcaaaccngt gggcacncag agaaccctac tctgtaataa 360
caatgaggaa tagccacggg gatctccagc accaaatctc tccatgttnt tccagagctc 420
ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tcctctgn 467

```

<210> 76

<211> 400

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(400)

<223> n = A,T,C or G

<400> 76

```

aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctgcgcgtac 60
tctctctttc tggcctggag gctatccagc gtactccaaa gattcaggtt tactcacgtc 120
atccagcaga gaatggaaag tcaaatttcc tgaattgcta tgtgtctggg ttctatccat 180
ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagtg gagcattcag 240
acttgtcttt cagcaaggac tgggtcttct atctcttgta ctacactgaa ttcaccccca 300
ctgaaaaaga tgagtatgcc tggcgtgtga accatgtgac tttgtcacag cccaagatng 360
ttnagtggga tcganacatg taagcagcan catgggaggt 400

```

<210> 77

<211> 248

<212> DNA

<213> Homo sapien

<400> 77

```

ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60

```

```

ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgctgc      120
caggcactgt tcatctcagc ttttctgtcc ctttgctccc ggcaagcgct tctgctgaaa      180
gttcatactc ggagcctgat gtcttaacga ataaaggctc catgctccac ccgaaaaaaa      240
aaaaaaaaa                                     248

```

<210> 78

<211> 201

<212> DNA

<213> Homo sapien

<400> 78

```

actagtccag tgtggtggaa ttccattgtg ttggggcccaa cacaatggct acctttaaca      60
tcaccagac cccgccctgc ccgtgcccc cgtgctgct aacgacagta tgatgcttac      120
tctgctactc ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataatgcct      180
gatttaaaaa aaaaaaaaaa a                                     201

```

<210> 79

<211> 552

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (552)

<223> n = A,T,C or G

<400> 79

```

tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg      60
tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttaacttccct attctttatt      120
cctctttctt ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag      180
tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatacc attcaaaatt      240
atgcaagtta gtaattactc agggttaact aaattacttt aatatgctgt tgaacctact      300
ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga      360
taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta      420
ttcccaggaa tatgggggttc atttatgaat antacccggt anagaagttt tgantnaaac      480
cngttttggt taatacgtaa atatgtcctn aatnaacaag gcntgactta tttccaaaaa      540
aaaaaaaaa aa                                     552

```

<210> 80

<211> 476

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (476)

<223> n = A,T,C or G

<400> 80

```

acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga      60
ggggaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccttggcct      120
cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccttgttt      180
gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcaact      240
aggttaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac      300
tcttctaagt cctcttccag cctcactttg agtcctcctt ggggggttgat aggaantntc      360

```



```
tcttggcttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat 420
gctgaaaaaa ttaaaatggt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa 476
```

```
<210> 81
<211> 232
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1)...(232)
<223> n = A,T,C or G
```

```
<400> 81
tttttttttg tatgcentcn ctgtggngtt attgttgctg ccaccctgga ggagcccagt 60
ttctttctgta tctttctttt ctgggggatc ttcttggtc tgccctcca tccccagcct 120
ctcatcccca tcttgcaactt ttgctagggt tggaggcgct ttcttggtag cccctcagag 180
actcagtcag cggaataaag tcctaggggt ggggggtgtg gcaagccggc ct 232
```

```
<210> 82
<211> 383
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G
```

```
<400> 82
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc 60
agtaccagta ccaataacat gccagtgccg gtgccagcac cagtgggtggc ttcagtgctg 120
gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggg ggagctgggt 180
ccagcaccag tggcagctct ggtgcctgtg gtttctccta caagtgagat tttagatatt 240
gttaatcctg ccagtctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac 300
agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg 360
ccatttcaaa aaaaaaaaaa aaa 383
```

```
<210> 83
<211> 494
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1)...(494)
<223> n = A,T,C or G
```

```
<400> 83
accgaattgg gaccgctggc ttataagcga tcatgtcctc cagtattacc tcaacgagca 60
gggagatcga gtctatacgc tgaagaaatt tgacccgatg ggacaacaga cctgctcagc 120
ccatcctgct cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa 180
acgcttcaag gtgctcatga cccagcaacc gcgcctgtc ctctgagggt ccttaaactg 240
atgtcttttc tgccacctgt taccctcgg agactccgta accaaactct tcggactgtg 300
agccctgatg cctttttgcc agccatactc tttggcntcc agtctctcgt ggcgattgat 360
```

tatgcttgtg tgaggcaatc atggtggcat cacccatnaa gggaacacat ttganttttt 420
 tttcncatat ttttaattac naccagaata nttcagaata aatgaattga aaaactctta 480
 aaaaaaaaaa aaaa 494

<210> 84
 <211> 380
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(380)
 <223> n = A,T,C or G

<400> 84
 gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca 60
 agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag 120
 gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttctgg 180
 gcacaccctc ctgggggccc gccgggcacc tgcgtctccc agtatgcaa ctggctggtg 240
 gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg 300
 ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360
 agcgttnccg cctcatccgg 380

<210> 85
 <211> 481
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(481)
 <223> n = A,T,C or G

<400> 85
 gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc 60
 tnccatcgtc atactgtagg tttgccacca ctcctgcat cttggggcgg ctaatatcca 120
 ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg 180
 tgtgaaagga tctccagaag gagtgtcga tcttccccac acttttgatg actttattga 240
 gtcgattctg catgtccagc aggaggttgt accagctctc tgacagtgag gtcaccagcc 300
 ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggg gnagtctcac 360
 ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggnngaa 420
 aaagaacacc tcctggaagt gctngccgct cctcgctcent tgggtggnngc gcntnecctt 480
 t 481

<210> 86
 <211> 472
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(472)
 <223> n = A,T,C or G

<400> 86

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aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt      60
acttggaana gcaacttnaa gcctggacac tggattataa attcacaata tgcaacactt      120
taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg      180
ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct ttttttttga      240
cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcacttttct      300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg      360
atatntgagc ggaagantag cttttctact tcaccagaca caactccttt catattggga      420
tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg              472

```

<210> 87

<211> 413

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(413)

<223> n = A,T,C or G

<400> 87

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agaaaccagt atctctnaaa acaacctctc ataccttgtg gacctaatTT tgtgtgcgtg      60
tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttgta aaagcttatg      120
cctcttttgg atctatatct gtgaaagtgt taatgatctg ccataatgtc ttggggacct      180
ttgtcttctg tgtaaatggg actagagaaa acacctatnt tatgagtcaa tctagttngt      240
tttattcgac atgaaggaaa ttccagatn acaactnaa caaactctcc cttgactagg      300
ggggacaaaag aaaagcnaaa ctgaacatna gaaacaattn cctggtgaga aattncataa      360
acagaaattg ggtngtatat tgaaanannng catcattnaa acgttttttt ttt              413

```

<210> 88

<211> 448

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(448)

<223> n = A,T,C or G

<400> 88

```

cgcagcgggt cctctctatc tagctccagc ctctcgctg ccccaactccc cgcgtcccgc      60
gtcctagccn accatggccg ggccccctgc cgccccctgc ctctgctgg ccatcctggc      120
cgtggccccg gccgtgagcc ccgcggcccg ctccagctcc ggcaagccgc cgcgcctggg      180
gggaggccca tggaccccg cgtggaagaag aagggtgtgc gcgtgcaact gactttgccg      240
tcggcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgctgcag gttgtgccgc      300
cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng      360
tttaccagaa ccnagccaat tngaacaatt nccccctcat aacagccccct tttaaaaagg      420
gaancantcc tgntcttttc caaatttt              448

```

<210> 89

<211> 463

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(463)

<223> n = A,T,C or G

<400> 89

gaattttgtg cactggccac tgtgatggaa ccattggggcc aggatgcttt gagtttatca	60
gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc	120
agaggtctag gtctgcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt	180
ctcagtgaca agttnnttct gatgcgaagt tctnattcca gtgttttagt cctttgcatc	240
tttnatgtn agacttgcct ctntnaaatt gcttttgtnt tctgcaggta ctatctgtgg	300
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn	360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn	420
aattcnnana anttcagntn tcatacaaca naacngganc ccc	463

<210> 90

<211> 400

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(400)

<223> n = A,T,C or G

<400> 90

agggattgaa ggtctnttnt actgtcggac tgttcancca ccaactctac aagttgctgt	60
cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaaciaat	120
tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttccact	180
tcctttgtta agacttcac tcgttaaagtc ttaagttttg tagaaaggaa tttaattgct	240
cgttctctaa caatgtcttc tccttgaagt atttggctga acaaccacc tnaagtcct	300
ttgtgcatcc attttaaata tacttaatag ggcattggtt cactagggtta aattctgcaa	360
gagtcactctg tctgcaaaag ttgcgttagt atatctygca	400

<210> 91

<211> 480

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(480)

<223> n = A,T,C or G

<400> 91

gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact	60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac	120
atgcctcttt gactaccgtg tgccagtgtc ggtgattctc acacacctcc nncgctctt	180
tgtggaaaaa ctggcacttg nctggaacta gcaagacatc acttacaaat tcacccacga	240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt	300
tgtcaatact aaccgctgg tttgcctcca tcacatttgt gatctgtagc tctggataca	360
tctctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt	420
ngatcagggt cccatttccc agtccgaatg ttcacatggc atatnttact tccccaaaa	480

<210> 92

<211> 477

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 92

atacagccca	natcccacca	cgaagatgcg	cttggtgact	gagaacctga	tgcggtcact	60
ggtcccgtg	tagccccagc	gactctccac	ctgctggaag	cggttgatgc	tgcactcctt	120
cccacgcagg	cagcagcggg	gccggtcaat	gaactccact	cgtggcttgg	ggttgacggt	180
taantgcagg	aagaggctga	ccacctcgcg	gtccaccagg	atgcccgaact	gtgcgggacc	240
tgcagcgaaa	ctcctcgatg	gtcatgagcg	ggaagcgaat	gangcccagg	gccttgccca	300
gaaccttccg	cctgttctct	ggcgtcacct	gcagctgctg	ccgctnacac	tcggcctcgg	360
accagcggac	aaacggcgtt	gaacagccgc	acctcacgga	tgcccantgt	gtcgcgctcc	420
aggaacggcn	ccagcgtgtc	caggtcaatg	tcggtgaanc	ctccgcgggt	aatggcg	477

<210> 93

<211> 377

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(377)

<223> n = A,T,C or G

<400> 93

gaacggctgg	accttgccctc	gcattgtgct	gctggcagga	ataccttggc	aagcagctcc	60
agtcgcgagca	gccccagacc	gctgccgccc	gaagctaagc	ctgcctcttg	ccttccccctc	120
cgcttcaatg	cagaaccant	agtgggagca	ctgtgttttag	agttaagagt	gaacactgtn	180
tgattttact	tgggaatttc	ctctgttata	tagcttttcc	caatgctaata	ttccaaacaa	240
caacaacaaa	ataacatggt	tgctgttna	gttgtataaa	agtangtgat	tctgtatnta	300
aagaaaatat	tactgttaca	tatactgctt	gcaanttctg	tattttattgg	tnctctggaa	360
ataaatatat	tattaaa					377

<210> 94

<211> 495

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(495)

<223> n = A,T,C or G

<400> 94

ccctttgagg	ggttaggggc	cagttcccag	tggaagaaac	aggccaggag	aantgcgtgc	60
cgagctgang	cagatttccc	acagtgaccc	cagagccctg	ggctatagtc	tctgaccctt	120
ccaaggaaaag	accaccttct	ggggacatgg	gctggagggc	aggacctaga	ggcaccaagg	180
gaaggcccca	ttccggggct	gttccccgag	gaggaaggga	aggggctctg	tgtgcccccc	240
acgaggaana	ggccctgant	cctgggatca	nacaccctt	cacgtgtatc	cccacacaaa	300
tgcaagctca	ccaaggtccc	ctctcagtc	cttccctaca	ccctgaacgg	ncactggccc	360
acacccacc	agancacca	cccgccatgg	ggaatgtnc	caaggaatcg	cngggcaacg	420
tggactctng	tcccnaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	480

aaaaaaaaana aaaaaa

495

<210> 95
 <211> 472
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(472)
 <223> n = A,T,C or G

<400> 95

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ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc      60
cctctggaag ccttgcgcag agcggacttt gtaattgttg gagaataact gctgaatttt      120
tagctgtttt gagttgattc gcaccactgc accacaactc aatatgaaaa ctatttnact      180
tatttattat cttgtgaaaa gtatacaatg aaaattttgt tcatactgta ttatcaagt      240
atgatgaaaa gcaatagata tatattcttt tattatgtnn aattatgatt gccattatta      300
atcggcaaaa tgtggagtgt atgttctttt cacagtaata tatgcctttt gtaacttcac      360
ttggttattt tattgtaaat gaattacaaa attcttaatt taagaaaatg gtangttata      420
tttanttcan taatttcttt ccttgtttac gttaattttg aaaagaatgc at              472

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<210> 96
 <211> 476
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(476)
 <223> n = A,T,C or G

<400> 96

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ctgaagcatt tcttcaaact tntctacttt tgtcattgat acctgtagta agttgacaat      60
gtggtgaaat ttcaaaatta tatgtaactt ctactagttt tactttctcc cccaagtctt      120
ttttaactca tgattttttac acacacaatc cagaacttat tatatagcct ctaagtcttt      180
attcttcaca gtagatgatg aaagagtccct ccagtgtctt gngcanaatg ttctagntat      240
agctggatac atacngtggg agttctataa actcatacct cagtgggact naaccaaatt      300
tgtgttagtc tcaattccta ccacactgag ggagcctccc aaatcactat attcttatct      360
gcaggtactc ctccagaaaa acngacaggg caggcttgca tgaaaaagtn acatctgcgt      420
tacaaagtct atcttcttca nangtctgtn aaggaacaat ttaatcttct agcttt      476

```

<210> 97
 <211> 479
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(479)
 <223> n = A,T,C or G

<400> 97

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actctttcta atgctgatat gatcttgagt ataagaatgc atatgtcact agaatggata      60
aaataatgct gcaaacctaa tgttcttatg caaaatggaa cgctaataaa acacagctta      120

```

caatcgcaaa	tcaaaaactca	caagtgtctca	tctgtttgtag	atctagtgtgta	ataagactta	180
gattgtgtctc	cttcggatat	gattgtttct	canatcttgg	gcaatnttcc	ttagtcaaat	240
caggctacta	gaattctgtt	attggatatn	tgagagcatg	aaatttttaa	naatacactt	300
gtgattatna	aattaatcac	aaatttcact	tatacctgct	atcagcagct	agaaaaacat	360
ntnnttttta	natcaaagta	ttttgtgttt	ggaantgtnn	aatgaaatc	tgaatgtggg	420
ttcnatctta	ttttttcccn	gacnactant	tnctttttta	gggnctatcc	tgancatc	479

<210> 98

<211> 461

<212> DNA

<213> Homo sapien

<400> 98

agtgacttgt	cctccaacaa	aaccccttga	tcaagtttgt	ggcactgaca	atcagacctt	60
tgctagtctc	tgctactat	tcgtactaa	atgcagactg	gaggggacca	aaaaggggca	120
tcaactccag	ctggattatt	ttggagcctg	caaactctatt	cctacttgta	cggactttga	180
agtgattcag	tttcctctac	ggatgagaga	ctggctcaag	aatacctca	tgacgcttta	240
tgaagccact	ctgaacacgc	tggttatcta	gatgagaaca	gagaaataaa	gtcagaaaat	300
ttacctggag	aaaagaggct	ttggctgggg	accatcccat	tgaaccttct	cttaaggact	360
ttaagaaaaa	ctaccacatg	ttgtgtatcc	tggtgccggc	cgtttatgaa	ctgaccaccc	420
tttggataaa	tcttgacgct	cctgaacttg	ctcctctgcg	a		461

<210> 99

<211> 171

<212> DNA

<213> Homo sapien

<400> 99

gtggcgcgc	gcaggtgttt	cctcgtaccg	cagggccccc	tcccttcccc	aggcgctccct	60
cggcgctct	gcgggcccga	ggaggagcgg	ctggcgggtg	gggggagtgt	gacccacccct	120
cggtgagaaa	agccttctct	agcgtatctga	gaggcgtgcc	ttgggggtac	c	171

<210> 100

<211> 269

<212> DNA

<213> Homo sapien

<400> 100

cggccgcaag	tgcaactcca	gctggggccg	tgccgacgaa	gattctgcca	gcagttgggtc	60
cgactgcgac	gacggcggcg	gcgacagtgc	caggtgcagc	gcgggcgcct	ggggtcttgc	120
aaggctgagc	tgacgccgca	gaggtcgtgt	cacgtccac	gacctgacg	ccgtcgggga	180
cagccggaac	agagcccggg	gaagcgggag	gcctcgggga	gcccctcggg	aagggcgggc	240
cgagagatac	gcaggtgcag	gtggccgcc				269

<210> 101

<211> 405

<212> DNA

<213> Homo sapien

<400> 101

tttttttttt	ttttggaatc	tactgcgagc	acagcaggtc	agcaacaagt	ttatcttgca	60
gctagcaagg	taacagggta	gggcatgggt	acatgttcag	gtcaacttcc	tttgtcgtgg	120
ttgattgggt	tgtctttatg	ggggcggggg	ggggtagggg	aaacgaagca	aataacatgg	180
agtgggtgca	ccctccctgt	agaacctggt	tacaaagctt	ggggcagttc	acctgggtctg	240
tgaccgtcat	tttcttgaca	tcaatgttat	tagaagtcag	gatatctttt	agagagtcca	300

ctgttctgga gggagattag gggttcttgc caaatccaac aaaatccact gaaaaagttg 360
 gatgatcagt acgaataccg aggcattatc tcatatcggt ggcca 405

<210> 102

<211> 470

<212> DNA

<213> Homo sapien

<400> 102

tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
ggcacttaat	ccatttttat	ttcaaaatgt	ctacaaattt	aatcccat	tacgggtatt	120
tcaaaatcta	aattattcaa	attagccaaa	tccttaccaa	ataatacca	aaaatcaaaa	180
atatacttct	ttcagcaaac	ttgttacata	aattaaaaaa	atatatacgg	ctgggtgttt	240
caaagtacaa	ttatcttaac	actgcaaaac	ttttaaggaa	ctaaaataaa	aaaaaacact	300
ccgcaaaagt	taaagggaac	aacaaattct	tttacaacac	cattataaaa	atcatatctc	360
aaatcttagg	ggaatatata	cttcacacgg	gatcttaact	tttactcact	ttgtttattt	420
ttttaaacca	ttgtttgggc	ccaacacaat	ggaatccccc	ctggactagt		470

<210> 103

<211> 581

<212> DNA

<213> Homo sapien

<400> 103

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaatggaaa	ctgccttaga	tacataatc	ttaggaatta	gcttaaaatc	tgctaaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaatc	240
atttttcttg	tctttaaaat	tatctaattc	ttccattttt	tccttatcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaca	ggaagagaaa	tggcacacaa	aacaaacatt	ttatattcat	atctctacct	420
acgttaataa	aatagcattt	tgtgaagcca	gctcaaaaga	aggcttagat	ccttttatgt	480
ccattttagt	cactaaacga	tatcaaagt	ccagaatgca	aaagggttgt	gaacatttat	540
tcaaaagcta	atataagata	tttcacatac	tcatctttct	g		581

<210> 104

<211> 578

<212> DNA

<213> Homo sapien

<400> 104

tttttttttt	tttttttttt	tttttctctt	cttttttttt	gaaatgagga	tcgagttttt	60
cactctctag	atagggcatg	aagaaaactc	atctttccag	ctttaaaata	acaatcaaat	120
ctcttatgct	atatcatatt	ttaagttaaa	ctaagtgtc	actggcttat	cttctcctga	180
aggaaatctg	ttcattcttc	tcattcatat	agttatatca	agtactacct	tgcatattga	240
gaggtttttt	ttctctatct	acacatatat	ttccatgtga	atttgtatca	aacctttatt	300
ttcatgcaaa	ctagaaaata	atgtttcttt	tgcataagag	aagagaacaa	tatagcatta	360
caaaaactgct	caaattgttt	gttaagttat	ccattataat	tagttggcag	gagctaatac	420
aatcacatt	tacgacagca	ataataaaac	tgaagtacca	gttaaatatc	caaaaataatt	480
aaaggaacat	ttttagcctg	ggtataatta	gctaattcac	tttacaagca	tttattagaa	540
tgaattcaca	tgttattatt	cctagcccaa	cacaatgg			578

<210> 105

<211> 538

<212> DNA

<213> Homo sapien

<400> 105

tttttttttt	tttttcagta	ataatcagaa	caatatttat	ttttatattt	aaaattcata	60
gaaaagtgcc	ttacatttaa	taaaagtttg	tttctcaaag	tgatcagagg	aattagatat	120
gtcttgaaca	ccaatattaa	tttgaggaaa	atacaccaaa	atacattaag	taaattattt	180
aagatcatag	agcttgtaag	tgaaaagata	aaatttgacc	tcagaaactc	tgagcattaa	240
aaatccacta	ttagcaaata	aattactatg	gacttcttgc	tttaattttg	tgatgaatat	300
ggggtgtcac	tggtaaacca	acacattctg	aaggatacat	tacttagtga	tagattctta	360
tgtactttgc	taatacgtgg	atatgagttg	acaagtttct	ctttcttcaa	tcttttaagg	420
ggcgagaaat	gaggaagaaa	agaaaaggat	tacgcatact	gttctttcta	tggaaggatt	480
agatatgttt	cctttgccaa	tattaaaaaa	ataataatgt	ttactactag	tgaaacccc	538

<210> 106

<211> 473

<212> DNA

<213> Homo sapien

<400> 106

tttttttttt	tttttagtc	aagtttctat	ttttattata	attaaagtct	tggtcatttc	60
atttatttagc	tctgcaactt	acataatttaa	attaaagaaa	cgttttagac	aactgtacaa	120
tttataaatg	taaggtgcc	ttattgagta	atataattcct	ccaagagtgg	atgtgtccct	180
tctcccacca	actaatgaac	agcaacatta	gtttaatttt	attagtagat	atacactgct	240
gcaaacgcta	attctcttct	ccatcccat	gtgatattgt	gtatatgtgt	gagttggtag	300
aatgcatcac	aatctacaat	caacagcaag	atgaagctag	gctgggcttt	cggtgaaaat	360
agactgtgtc	tgtctgaatc	aaatgatctg	acctatcctc	ggtggcaaga	actcttcgaa	420
ccgcttcctc	aaaggcgctg	ccacatttgt	ggctctttgc	acttggttca	aaa	473

<210> 107

<211> 1621

<212> DNA

<213> Homo sapien

<400> 107

cgccatggca	ctgcagggca	tctcggtcat	ggagctgtcc	ggcctggccc	cgggcccgtc	60
ctgtgctatg	gtcctggctg	acttcggggc	gcgtgtggta	cgcgtggacc	ggcccggctc	120
ccgctacgac	gtgagccgct	tgggcccggg	caagcgctcg	ctagtgtctg	acctgaagca	180
gccgcgggga	gccgcgctgc	tgcggcgtct	gtgcaagcgg	tcggatgtgc	tgctggagcc	240
cttcgcggc	ggtgtcatgg	agaaaactcca	gctgggccc	gagattctgc	agcgggaaaa	300
tccaaggctt	atztatgcca	ggctgagtg	atltggccag	tcaggaagct	tctgccggtt	360
agctggccac	gatatcaact	atltggcttt	gtcaggtgtt	ctctcaaaaa	ttggcagaag	420
tggtgagaat	ccgtatgcc	cgctgaatct	cctggctgac	tttgctggtg	gtggccttat	480
gtgtgactg	ggcattataa	tggtctttt	tgaccgcaca	cgcactgaca	agggtcaggt	540
cattgatgca	aatatgggtg	aaggaacagc	atatttaagt	tcttttctgt	ggaaaactca	600
gaaatcgagt	ctgtgggaag	cacctcgagg	acagaacatg	ttggatgggtg	gagcaccttt	660
ctatacgact	tacaggacag	cagatgggga	attcatggct	gttgagcaa	tagaacccca	720
gttctacgag	ctgctgatca	aaggacttgg	actaaagtct	gatgaacttc	ccaatcagat	780
gagcatggat	gattggccag	aaatgaagaa	gaagtttgca	gatgtatttg	caaagaagac	840
gaaggcagag	tggtgtcaaa	tctttgacgg	cacagatgcc	tgtgtgactc	cgggtctgac	900
ttttgaggag	gttggttcac	atgatcaca	caaggaacgg	ggctcgttta	tcaccagtga	960
ggagcaggac	gtgagccccc	gccctgcacc	tctgctgtta	aacaccccag	ccatcccttc	1020
tttcaaaagg	gatcctttca	taggagaaca	cactgaggag	atacttgaag	aatttggtat	1080
cagccgcgaa	gagatttatc	agcttaactc	agataaaatc	attgaaagta	ataaggtaaa	1140
agctagtctc	taacttcag	gccacggct	caagtgaatt	tgaatactgc	atttacagtg	1200
tagagtaaca	cataacattg	tatgcatgga	aacatggagg	aacagtatta	cagtgtccta	1260

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ccactctaatt caagaaaaga attacagact ctgattctac agtgatgatt gaattctaaa 1320
aatgggttattc attagggctt ttgatttata aaactttggg tacttataact aaattatggt 1380
agttattctg ccttccagtt tgcttgatat atttgttgat attaagattc ttgacttata 1440
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atttacactc ttgattctac aatgtagaaa atgaggaaat gccacaaatt gtatgggtgat 1560
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a 1621

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<210> 108
 <211> 382
 <212> PRT
 <213> Homo sapien

<400> 108

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Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1      5      10      15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20      25      30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35      40      45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50      55      60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65      70      75      80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85      90      95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100     105     110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115     120     125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130     135     140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145     150     155     160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165     170     175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180     185     190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195     200     205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210     215     220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225     230     235     240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245     250     255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
260     265     270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
275     280     285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
290     295     300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
305     310     315     320
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala

```

```
<210> 109
<211> 1524
<212> DNA
<213> Homo sapien
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ggcacgaggc	tgcgccaggg	cctgagcgga	ggcgggggca	gcctcgccag	cggggggccc	60
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cagtgcgacc	tagtggctct	cacctgcttc	ctcctgggcg	tgggctgcgc	gctgaccccg	180
ggtttgtacc	acctgggccg	cactgtcctc	tgcacgact	tcatggtttt	cacggtgcgc	240
ctgcttcaca	tcttcacggg	caacaaacag	ctggggccca	agatcgtcat	cgtgagcaag	300
atgatgaagg	acgtgttctt	cttctcttct	ttctctggcg	tgtggctggt	agcctatggc	360
gtggccacgg	aggggctcct	gaggccacgg	gacagtgact	tcccaagtat	cctgcgcgc	420
gtcttctacc	gtccctacct	gcagatcttc	gggcagattc	cccaggagga	catggacgtg	480
gccctcatgg	agcacagcaa	ctgctcgtcg	gagcccggt	tctgggcaca	ccctcctggg	540
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acattcgcca	aagtacagg	caacagcgat	ctctactgga	aggcgcagc	ttaccgcctc	720
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gagcgtctga	agcgcacgtc	ccagaagggtg	gacttggcac	tgaacacgct	gggacacatc	1020
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cagaggaana	aaaaaaaaaa	aaaa				1524

```
<210> 110
<211> 3410
<212> DNA
<213> Homo sapien
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gggaaccagc	ctgcacgcgc	tggctccggg	tgacagccgc	gcgctctggc	caggatctga	60
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aagctggacc	ggcaccaaag	ggctggcaga	aatgggcgcc	tggctgattc	ctaggcagtt	180
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tggcctggag	gtgtgtttgg	ccgcaggcat	cacctatgtg	ccgcctctgc	tgctggaagt	420
gggggtagag	gagaagttca	tgaccatggt	gctgggcatt	ggtccagtgc	tgggcctggt	480

ctgtgtcccg	ctcctaggct	cagccagtga	ccactggcgt	ggacgctatg	gcccgcgccg	540
gcccttcac	tgggcactgt	ccttgggcat	cctgtgagc	ctctttctca	tcccaagggc	600
cggctggcta	gcagggtgc	tgtgcccga	tccagggcc	ctggagctgg	cactgctcat	660
cctgggcgtg	gggctgctgg	acttctgtgg	ccagggtgtc	ttcactccac	tggaggccct	720
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tagcgggggtg	aatattttat	actgtaagt	agcaatcaga	gtataatgtt	tatgggtgaca	3300
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aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaataa	aaaaaaaaaa		3410

<210> 111

<211> 1289

<212> DNA

<213> Homo sapien

<400> 111

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gtggagcctc agcagttccc tctttcagaa ctactgccca agagccctga acaggagcca      120
ccatgcagtg cttcagcttc attaagacca tgatgatcct cttcaatttg ctcactcttc      180
tgtgtggtgc agccctggtg gcagtgggca tctgggtgtc aatcgatggg gcatcctttc      240
tgaagatctt cgggccactg tcgtccagtg ccatgcagtt tgtcaacgtg ggctacttcc      300
tcacgcagc cggcggtgtg gtctttgtct ttggtttctt gggctgctat ggtgctaaga      360
ctgagagcaa gtgtgccctc gtgacgttct tcttcactct cctcctcatc ttcattgctg      420
aggttgcagc tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt      480
tgctggtagt gcctgccatc aagaaagatt atggttccca ggaagacttc actcaagtgt      540
ggaacaccac catgaaaggg ctcaagtgtc gtggcttcac caactatacg gattttgagg      600
actcacccta cttcaaagag aacagtgcct ttccccatt ctgttgcaat gacaacgtca      660
ccaacacagc caatgaaacc tgcaccaagc aaaaggctca cgacaaaaaa gtagaggggt      720
gcttcaatca gcttttgtat gacatccgaa ctaatgcagt caccgtgggt ggtgtggcag      780
ctggaattgg gggcctcgag ctggctgccca tgattgtgtc catgtatctg tactgcaatc      840
tacaataagt ccacttctgc ctctgccact actgctgccca catgggaact gtgaagaggc      900
accctggcaa gcagcagtga ttgggggagg ggacaggatc taacaatgtc acttgggcca      960
gaatggacct gccctttctg ctccagactt ggggctagat agggaccact ccttttagcg     1020
atgcctgact ttccttccat tgggtgggtgg atgggtgggg ggcatccag agcctctaag     1080
gtagccagtt ctgttgccca ttccccagt ctattaaacc cttgatatgc cccctaggcc     1140
tagtgggtgat cccagtgtct tactggggga tgagagaaag gcattttata gcctgggcat     1200
aagtgaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc     1260
tgttacaatg ttaaaaaaaaa aaaaaaaaaa                                     1289

```

<210> 112

<211> 315

<212> PRT

<213> Homo sapien

<400> 112

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Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1          5          10          15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
          20          25          30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
          35          40          45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
          50          55          60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
          65          70          75          80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
          85          90          95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
          100          105          110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
          115          120          125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
          130          135          140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
          145          150          155          160
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
          165          170          175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
          180          185          190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu

```

195 200 205
 His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
 210 215 220
 Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
 225 230 235 240
 Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
 245 250 255
 Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
 260 265 270
 Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
 275 280 285
 Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
 290 295 300
 Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
 305 310 315

<210> 113

<211> 553

<212> PRT

<213> Homo sapien

<400> 113

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 1 5 10 15
 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30
 Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
 35 40 45
 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
 50 55 60
 Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
 65 70 75 80
 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
 85 90 95
 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
 100 105 110
 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
 115 120 125
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205
 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg

```

      260      265      270
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
      275      280      285
Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
      290      295      300
Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
305      310      315      320
Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
      325      330      335
Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
      340      345      350
Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
      355      360      365
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
      370      375      380
Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
385      390      395      400
Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
      405      410      415
Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
      420      425      430
Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
      435      440      445
Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
      450      455      460
Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
465      470      475      480
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
      485      490      495
Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
      500      505      510
Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
      515      520      525
Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
      530      535      540
Lys Ser Asp Leu Ala Lys Tyr Ser Ala
545      550

```

<210> 114

<211> 241

<212> PRT

<213> Homo sapien

<400> 114

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Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
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Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
      20      25      30
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
      35      40      45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
      50      55      60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
65      70      75      80
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile

```

```

      85              90              95
Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
      100              105              110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
      115              120              125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
      130              135              140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
      145              150              155              160
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
      165              170              175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
      180              185              190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
      195              200              205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
      210              215              220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
      225              230              235              240
Gln

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<210> 115
 <211> 366
 <212> DNA
 <213> Homo sapien

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<400> 115
gctctttctc tccctcctc tgaatttaat tctttcaact tgcaatttgc aaggattaca      60
catttcactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac      120
ttggtttggt aatccatctt gctttttccc cattgggaact agtcattaac ccatctctga      180
actggtagaa aaacatctga agagctagtc tatcagcatc tgacagggtga attggatggt      240
tctcagaacc atttcacca gacagcctgt ttctatcctg tttaataaat tagtttgggt      300
tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt      360
ttagtc

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<210> 116
 <211> 282
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(282)
 <223> n = A,T,C or G

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<400> 116
acaaagatga accatttcct atattatagc aaaattaaaa tctaccgta ttctaatt      60
gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa      120
agactttact attttcatat tttaagacac atgatttata ctattttagt aacctgggtc      180
atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt      240
tcaatctnga actatctana tcacagacat ttctattcct tt

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<210> 117
 <211> 305

<212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (305)
 <223> n = A,T,C or G

<400> 117
 acacatgtcg cttcactgcc ttcttagatg cttctgggtca acatanagga acagggacca 60
 tatttatcct ccctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120
 aataaggcaa aatatatgaa acaacagggtc tcgagatatt ggaaatcagt caatgaagga 180
 tactgatccc tgatcactgt cctaatagcag gatgtgggaa acagatgagg tcacctctgt 240
 gactgccccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat 300
 tgggt 305

<210> 118
 <211> 71
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (71)
 <223> n = A,T,C or G

<400> 118
 accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa 60
 aantcctggg t 71

<210> 119
 <211> 212
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (212)
 <223> n = A,T,C or G

<400> 119
 actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca 60
 gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac 120
 agtaagctgg cccttctaataaaaagaaaat tgaaagggtt ctcactaanc ggaattaant 180
 aatggantca aganactccc aggcctcagc gt 212

<210> 120
 <211> 90
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (90)
 <223> n = A,T,C or G

<400> 120		
actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tgggtcttgcc		60
ctccgccggc gcagaacatg ctgggggtggt		90
<210> 121		
<211> 218		
<212> DNA		
<213> Homo sapien		
<220>		
<221> misc_feature		
<222> (1)...(218)		
<223> n = A,T,C or G		
<400> 121		
tgtancgtga anacgacaga naggggtgtc aaaaatggag aanccttgaa gtcattttga		60
gaataagatt tgctaaaaga tttgggggcta aaacatgggt attgggagac atttctgaag		120
atatncangt aaattangga atgaattcat ggttcttttg ggaattcctt tacgatngcc		180
agcatanact tcatgtgggg atancagcta cccttgta		218
<210> 122		
<211> 171		
<212> DNA		
<213> Homo sapien		
<400> 122		
taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg		60
catttgttag ctcatggaac aggaagtcgg atgggtggggc atcttcagtg ctgcatgagt		120
caccaccccg gcggggcat ctgtgccaca ggtccctgtt gacagtgcgg t		171
<210> 123		
<211> 76		
<212> DNA		
<213> Homo sapien		
<220>		
<221> misc_feature		
<222> (1)...(76)		
<223> n = A,T,C or G		
<400> 123		
tgtagcgtga agacnacaga atgggtgtgtg ctgtgctatc caggaacaca tttattatca		60
ttatcaanta ttgtgt		76
<210> 124		
<211> 131		
<212> DNA		
<213> Homo sapien		
<400> 124		
acctttccccc aaggccaatg tcctgtgtgc taactggccg gctgcaggac agctgcaatt		60
caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg		120
ttaagatttg t		131

<210> 125
<211> 432
<212> DNA
<213> Homo sapien

<400> 125
acttttatcta ctggctatga aatagatggt ggaaaattgc gttaccaact ataccactgg 60
cttgaaaaag aggtgatagc tcttcagagg acttgtgact tttgctcaga tgctgaagaa 120
ctacagtctg catttggcag aaatgaagat gaatttgat taaatgagga tgctgaagat 180
ttgectcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg 240
ctcttgaggt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc 300
catggtgggg gtcttgcacg tgtaagaatg gaattgattt tgcttttgca agaattctcag 360
caggaaacat cagaaccact attttctagc cctctgtcag agcaaaccctc agtgcctctc 420
ctctttgctt gt 432

<210> 126
<211> 112
<212> DNA
<213> Homo sapien

<400> 126
acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60
agtaagaatg atatttcccc ccagggatca ccaaatttt ataaaaattt gt 112

<210> 127
<211> 54
<212> DNA
<213> Homo sapien

<400> 127
accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128
<211> 323
<212> DNA
<213> Homo sapien

<400> 128
acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc 60
acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca 120
ttctctctga agtctaggtt acccattttg gggaccatt ataggcaata aacacagtgc 180
ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcctttt tcttagcctt 240
ttcctgcaaa aggtcactc agtcccttgc ttgctcagtg gactgggctc cccagggcct 300
aggctgcctt cttttccatg tcc 323

<210> 129
<211> 192
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(192)
<223> n = A,T,C or G

<400> 129
 acatacatgt gtgtatatatt ttaaatatca cttttgtatc actctgactt tttagcatac 60
 tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc 120
 tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg 180
 gataaacaaa gt 192

<210> 130
 <211> 362
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(362)
 <223> n = A,T,C or G

<400> 130
 cccctttttaa tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60
 tataatgacg caacaaaaag gtgctgttta gtcctatggt tcagtttatg cccctgacaa 120
 gtttccattg tgttttgccg atcttctggc taatcgtggt atcctccatg ttattagtaa 180
 ttctgtattc ctttttgta acgcctggta gatgtaacct gctangaggc taactttata 240
 cttatttaaa agctcttatt ttgtggcat taaaatggca atttatgtgc agcactttat 300
 tgcagcagga agcacgtgtg ggttggttgt aaagctcttt gctaacttta aaaagtaatg 360
 gg 362

<210> 131
 <211> 332
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(332)
 <223> n = A,T,C or G

<400> 131
 ctttttgaaa gatcgtgtcc actcctgtgg acatcttggt ttaatggagt ttcccatgca 60
 gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga 120
 gttctcccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc 180
 ttctgaacta gattaaggca gcttgtaaat ctgatgtgat ttggtttatt atccaactaa 240
 cttccatctg ttatcactgg agaaagccca gactcccan gacnggtacg gattgtgggc 300
 atanaaggat tgggtgaagc tggcgttgtg gt 332

<210> 132
 <211> 322
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(322)
 <223> n = A,T,C or G

<400> 132
 acttttgcca tttgtatat ataaacaatc ttgggacatt ctctgaaaa ctaggtgtcc 60

```

agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat    120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt    180
tttagcaagt taaaatgaan atgacaggaa aggcttattt atcaacaaag agaagagttg    240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct aggggaagcct    300
gtaacaatct acaattggtc ca                                           322

```

<210> 133

<211> 278

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 133

```

acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt    60
cttgtttttc tttccatctg gctcctgggt tgacaatttg tggaaacaac tctattgcta    120
ctatttaaaa aaaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg    180
ctattcctgt tttgtcaaag aaattatatt tttcaaaata tgtntatttg tttgatgggt    240
cccacgaaac actaataaaa accacagaga ccagcctg                               278

```

<210> 134

<211> 121

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(121)

<223> n = A,T,C or G

<400> 134

```

gtttanaaaa cttgttttagc tccatagagg aaagaatgtt aaactttgta ttttaaaaca    60
tgattctctg aggttaaact tgggtttcaa atgttatatt tacttgtatt ttgcttttgg    120
t                                                                    121

```

<210> 135

<211> 350

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(350)

<223> n = A,T,C or G

<400> 135

```

acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctataacc    60
atancaagtg gtgactgggt aagcgtgcga caaaggtcag ctggcacatt acttgtgtgc    120
aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtagtcca    180
gggtgcccc caactcctgc agcgcctcct ctgtgccagn ccctgnaagg aactttcgct    240
ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag    300
ttcccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt             350

```

<210> 136
 <211> 399
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(399)
 <223> n = A,T,C or G

<400> 136
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60
 gctgtgattg tatccgaata ntcctcgtga gaaaagataa tgagatgacg tgagcagcct 120
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180
 cctggcgggc agccagccag ccacagggtg gcttcttcct tttgtggtga caacccaag 240
 aaaactgcag aggcccaagg tcagggtgna gtgggtangt gaccataaaa caccagggtgc 300
 tcccaggaac ccgggcaaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360
 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137
 <211> 165
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(165)
 <223> n = A,T,C or G

<400> 137
 actggtgtgg tngggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60
 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120
 ttggctggtc ccactggtgg tcactgtcat tggtgggggt cctgt 165

<210> 138
 <211> 338
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(338)
 <223> n = A,T,C or G

<400> 138
 actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60
 ttaactttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccac 120
 tgctgggagc tctcccatgc cttccacagt gaaagggtt gagaaaaatc acatccaatg 180
 tcatgtgttt ccagccacac caaaagggtc ttgggggtgga gggctggggg catananggt 240
 cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa 300
 aaaaactgat gccttttttt tttttttttg taaaattc 338

<210> 139
 <211> 382

<212> DNA

<213> Homo sapien

<400> 139

gggaatcttg	gtttttggca	tctggtttgc	ctatagccga	ggccactttg	acagaacaaa	60
gaaagggact	tcgagtaaga	aggtgattta	cagccagcct	agtgcccga	gtgaaggaga	120
attcaaacag	acctcgtcac	tcctgggtgtg	agcctgggtcg	gctcaccgcc	tatcatctgc	180
atttgcttta	ctcaggtgct	accggactct	ggccccgat	gtctgtagtt	tcacaggatg	240
ccttatttgt	ctttacacc	ccacagggcc	ccctacttct	tcggatgtgt	ttttaataat	300
gtcagctatg	tgccccatcc	tccttcacgc	cctccctccc	tttcctacca	ctgctgagtg	360
gcctggaact	tgtttaaagt	gt				382

<210> 140

<211> 200

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (200)

<223> n = A,T,C or G

<400> 140

accaaancct	ctttctgttg	tggtngattt	tactataggg	gtttngcttn	ttctaaanat	60
acttttcatt	taacancctt	tggttaagtgt	caggctgcac	tttgctccat	anaattattg	120
ttttcacatt	tcaacttgta	tggtgtgtgc	tcttanagca	ttggtgaaat	cacatatttt	180
atattcagca	taaaggagaa					200

<210> 141

<211> 335

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (335)

<223> n = A,T,C or G

<400> 141

actttatttt	caaaacactc	atatgttgca	aaaaacacat	agaaaaataa	agtttggtgg	60
gggtgctgac	taaacttcaa	gtcacagact	tttatgtgac	agattggagc	agggtttgtt	120
atgcatgtag	agaacccaaa	ctaatttatt	aaacaggata	gaaacaggct	gtctgggtga	180
aatggttctg	agaaccatcc	aattcacctg	tcagatgctg	atanactagc	tcttcagatg	240
tttttctacc	agttcagaga	tnggttaatg	actanttcca	atgggggaaa	agcaagatgg	300
attcacaac	caagtaattt	taaacaaaga	cactt			335

<210> 142

<211> 459

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (459)

<223> n = A,T,C or G

<400> 142

accagggttaa	tattgccaca	tatataccttt	ccaattgcgg	gctaaacaga	cgtgtatttta	60
gggttggtta	aagacaaccc	agcttaatat	caagagaaat	tgtgaccttt	catggagtat	120
ctgatggaga	aaacactgag	ttttgacaaa	tcttatttta	ttcagatagc	agtctgatca	180
cacatgggtcc	aacaacactc	aaataataaa	tcaaataatna	tcagatgtta	aagattggtc	240
ttcaaacatc	atagccaatg	atgccccgct	tgctataat	ctctccgaca	taaaaccaca	300
tcaaacacctc	agtggccacc	aaaccattca	gcacagcttc	cttaactgtg	agctgtttga	360
agctaccagt	ctgagcacta	ttgactatnt	ttttcangct	ctgaatagct	ctagggatct	420
cagcanggggt	gggaggaacc	agctcaacct	tggcgtant			459

<210> 143

<211> 140

<212> DNA

<213> Homo sapien

<400> 143

acatttcctt	ccaccaagtc	aggactcctg	gcttctgtgg	gagttcttat	cacctgaggg	60
aatccaaac	agtctctcct	agaaaggaat	agtgtcacca	acccaccca	tctccctgag	120
accatccgac	ttccctgtgt					140

<210> 144

<211> 164

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(164)

<223> n = A,T,C or G

<400> 144

acttcagtaa	caacatacaa	taacaacatt	aagtgtatat	tgccatcttt	gtcattttct	60
atctatacca	ctctcccttc	tgaaaacaan	aatcactanc	caatcactta	tacaaatttg	120
aggcaattaa	tccatatttg	ttttcaataa	ggaaaaaaag	atgt		164

<210> 145

<211> 303

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 145

acgtagacca	tccaactttg	tatttgtaat	ggcaaacatc	cagnagcaat	tcctaaacaa	60
actggagggt	atttataccc	aattatccca	ttcattaaca	tgccctcctc	ctcagggtat	120
gcaggacagc	tatcataagt	cggcccaggc	atccagatac	taccatttgt	ataaacttca	180
gtaggggagt	ccatccaagt	gacagggtct	atcaaaggag	gaaatggaac	ataagccag	240
tagtaaaatn	ttgcttagct	gaaacagcca	caaaagactt	accgccgtgg	tgattaccat	300
caa						303

<210> 146

<211> 327
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(327)
<223> n = A,T,C or G

<400> 146
actgcagctc aattagaagt ggtctctgac ttctcatcanc ttctccctgg gctccatgac 60
actggcctgg agtgactcat tgctctggtt gggtgagaga gctcctttgc caacaggcct 120
ccaagtacagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt 180
cctgaacagg gaggggtggga ggagccagca tggaacaagc tgccactttc taaagtagcc 240
agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300
taggggtgag ctgtgtgact ctatggt 327

<210> 147
<211> 173
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(173)
<223> n = A,T,C or G

<400> 147
acattgtttt tttagataa agcattgana gagctctcct taacgtgaca caatggaagg 60
actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120
atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt 173

<210> 148
<211> 477
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(477)
<223> n = A,T,C or G

<400> 148
acaaccactt tatctcatcg aatttttaac ccaaactcac tcactgtgcc tttctatcct 60
atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120
gccctactac ctgctgcaat aatcacattc ccttctgtgc ctgacctga agccattggg 180
gtggctcctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgctcac 240
nccanccac ctcaccgacc ccacccctct acacagctac ctccttgctc tctaacccca 300
tagattatnt ccaaattcag tcaattaagt tactattaac actctaccg acatgtccag 360
caccactggg aagccttctc cagccaacac acacacacac acacncacac acacacatat 420
ccaggcacag gctacctcat cttcacatc acccctttaa ttaccatgct atggtgg 477

<210> 149
<211> 207
<212> DNA

<213> Homo sapien

<400> 149

```
acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac      60
taacgtattt tagagagcca aggaagggtt ctgtggggag tgggatgtaa ggtggggcct      120
gatgataaat aagagtcagc caggtaagtg ggtggtgtgg tatgggcaca gtgaagaaca      180
tttcaggcag agggaacagc agtgaac                                     207
```

<210> 150

<211> 111

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(111)

<223> n = A,T,C or G

<400> 150

```
accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg      60
cacttaaatt tggtcagtgt ttggacttgt taactantgg catctttggg t              111
```

<210> 151

<211> 196

<212> DNA

<213> Homo sapien

<400> 151

```
agcgcggcag gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac      60
agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat      120
ggataccaac cggaaaaccc ctatcccgca cagcccactg tggccccac tgtctacgag      180
gtgcatccgg ctcaagt                                     196
```

<210> 152

<211> 132

<212> DNA

<213> Homo sapien

<400> 152

```
acagcacttt cacatgtaag aaggagagaaa ttccctaaatg taggagaaag ataacagaac      60
cttccccttt tcatctagtg gtggaaacct gatgctttat gttgacagga atagaaccag      120
gaggagttt gt                                             132
```

<210> 153

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(285)

<223> n = A,T,C or G

<400> 153

```
acaanacca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag      60
```

```

cttctgctct tatgtcctca tctgacaact ctttaccatt tttatcctcg ctcagcagga 120
gcacatcaat aaagtccaaa gtcttggaact tggccttggc ttggaggaag tcatcaacac 180
cctggctagt gaggggtgcgg cgccgctcct ggatgacggc atctgtgaag tcgtgcacca 240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt 285

```

```

<210> 154
<211> 333
<212> DNA
<213> Homo sapien

```

```

<400> 154
accacagtcc tgttgggcca gggcttcatg accctttctg tgaaaagcca tattatcacc 60
accccaaatt tttccttaa tctctttaa tgaaggggtc agcctcttga ctgcaaagac 120
cctaagccgg ttacacagct aactccact ggccttgatt tgtgaaattg ctgctgcctg 180
attggcacag gagtcgaagg tgttcagctc cctcctccg tggaaacgaga ctctgatttg 240
agtttcacaa attctcgggc cacctcgtca ttgctcctc gaaataaaat ccggagaatg 300
gtcaggcctg tctcatccat atggatcttc cgg 333

```

```

<210> 155
<211> 308
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(308)
<223> n = A,T,C or G

```

```

<400> 155
actggaaata ataaaaccca catcacagtg ttgtgtcaaa gatcatcagg gcatggatgg 60
gaaagtgctt tgggaactgt aaagtgccta acacatgatc gatgattttt gttataatat 120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagcccc 180
atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggct 240
gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtgta aggcattgctg 300
gccttggc 308

```

```

<210> 156
<211> 295
<212> DNA
<213> Homo sapien

```

```

<400> 156
accttgctcg gtgcttggaa catattagga actcaaaata tgagatgata acagtgccta 60
ttattgatta ctgagagaac tgtagacat ttagttgaag attttctaca caggaaactga 120
gaataggaga ttatgtttgg cctcatatt ctctcctatc ctccttgcct cattctatgt 180
ctaatatatt ctcaatcaaa taaggtttagc ataatcagga aatcgaccaa ataccaatat 240
aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat 295

```

```

<210> 157
<211> 126
<212> DNA
<213> Homo sapien

```

```

<400> 157
acaagtttaa atagtgtgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct 60

```

gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc 120
cttagt 126

<210> 158

<211> 442

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(442)

<223> n = A,T,C or G

<400> 158

accactggt cttgaaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg 60
aanccagcag gctgccccta gtcagtcctt ccttccagag aaaaagagat ttgagaaagt 120
gcctgggtaa ttcaccatta atttcctccc ccaaactctc tgagtcttcc cttaatatatt 180
ctggtggttc tgaccaaagc aggtcatggt ttgttgagca tttgggatcc cagtgaagta 240
natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtgg cagagtgggtg 300
ccaaccctgt tttcccagtc cacgtagaca gattcacagt gcggaattct ggaagctgga 360
nacagacggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg 420
tgttcattct ctgatgtcct gt 442

<210> 159

<211> 498

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(498)

<223> n = A,T,C or G

<400> 159

acttccaggt aacgttggtg tttccgttga gcctgaactg atgggtgacg ttgtaggttc 60
tccaacaaga actgaggttg cagagcgggt agggagagat gctgttccag ttgcacctgg 120
gctgctgtgg actgttggtg attcctcact acggcccaag gttgtggaac tggcanaaag 180
gtgtgtgtgt gganttgagc tcgggcggct gtggtagggt gtgggctctt caacaggggc 240
tgctgtgggt ccgggangtg aangtggtgt gtcacttgag cttggccagc tctggaaagt 300
antanattct tcctgaaggc cagcgcttgt ggagctggca ngggtcantg ttgtgtgtaa 360
cgaaccagtg ctgctgtggg tgggtgtana tcctccacaa agcctgaagt tatggtgtcn 420
tcaggtanaa atgtggtttc agtgtccctg ggcngctgtg gaaggttgta nattgtcacc 480
aagggaataa gctgtgggt 498

<210> 160

<211> 380

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(380)

<223> n = A,T,C or G

<400> 160

```

acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac      60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct      120
ggagcatggc atagaggaag ctganaaatg tggggtctga ggaagccatt tgagtctggc      180
cactagacat ctcatcagcc acttgtgtga agagatgccc catgacccca gatgcctctc      240
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg      300
gagaaaaatg gcagtttgac cgaacctgtt cacaacggtg gaggctgatt tctaacgaaa      360
cttgtagaat gaagcctgga                                     380

```

```

<210> 161
<211> 114
<212> DNA
<213> Homo sapien

```

```

<400> 161
actccacatc ccctctgagc aggcgggtgt cgttcaaggt gtatttggcc ttgcctgtca      60
cactgtccac tggccccctta tccacttggg gcttaatccc tcgaaagagc atgt          114

```

```

<210> 162
<211> 177
<212> DNA
<213> Homo sapien

```

```

<400> 162
actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa      60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt      120
tgggtgatata taacttggca ataaccagtc ctggtgatac ataaaactac tcactgt       177

```

```

<210> 163
<211> 137
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (137)
<223> n = A,T,C or G

```

```

<400> 163
catttataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac      60
canagaaggc agctacggct actcctacat cctggcgtgg gtggccttcg cctgcacctt      120
catcagcggc atgatgt                                     137

```

```

<210> 164
<211> 469
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (469)
<223> n = A,T,C or G

```

```

<400> 164
cttatcacia tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta      60
tgcaatgcat catgctatct catacctaag gaggagattc aaccaggaaa               120

```

```

tgcattggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt      180
gagacatgca cttgctacga aacagaaatt tcatgttgca cccttggttc tacacctgtg      240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg      300
gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct      360
tctagtaggc acagggctcc caggccaggc ctcatctccc tctggcctct aatagtcaat      420
gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt      469

```

<210> 165

<211> 195

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(195)

<223> n = A,T,C or G

<400> 165

```

acagtttttt ataatatcg acattgccgg cacttgtgtt cagtttcata aagctgggtg      60
atccgctgtc atccactatt ccttggttag agtaaaaatt attcttatag cccatgtccc      120
tgcaggccgc ccgcccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact      180
tcctctgaga tgagt      195

```

<210> 166

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 166

```

acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc      60
cgaggctgga gtccacacca ccggtgtagg tgtgctcaat cttgggcttg gcgcccacct      120
ttggagaagg gatatgctgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt      180
tttcagacc agcctgagca aggggaggat gttcagcttc agtcctcct tcgtcaggtg      240
gatccaacc tcgtctangg tccgtgggaa gctgggtgtc acntcaccta caacctgggc      300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt      360
nggggccttt ttggtgaact ttc      383

```

<210> 167

<211> 247

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(247)

<223> n = A,T,C or G

<400> 167

```

acagagccag accttgcca taaatgaanc agagattaag actaaacccc aagtcganat      60
tggagcagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc      120

```

tatanccata	cacagagcca	actctcaggc	caaggcnatg	gttggggcag	anccagagac	180
tcaatctgan	tccaaagtgg	tggctggaac	actgggtcatg	acanaggcag	tgactctgac	240
tgangtc						247

<210> 168

<211> 273

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (273)

<223> n = A,T,C or G

<400> 168

acttctaagt	tttctagaag	tggaaggatt	gtantcatcc	tgaaaatggg	tttacttcaa	60
aatccctcan	ccttggttctt	cacnactgtc	tatactgana	gtgtcatggt	tccacaaagg	120
gctgacacct	gagcctgnat	tttactcat	ccctgagaag	ccctttccag	taggggtgggc	180
aattcccaac	ttccttgcca	caagcttccc	aggttttctc	ccctggaaaa	ctccagcttg	240
agtcccagat	acactcatgg	gctgccttgg	gca			273

<210> 169

<211> 431

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (431)

<223> n = A,T,C or G

<400> 169

acagccttgg	cttccccaaa	ctccacagtc	tcagtgcaga	aagatcatct	tccagcagtc	60
agctcagacc	aggggtcaaag	gatgtgacat	caacagtttc	tggtttcaga	acagggttcta	120
ctactgtcaa	atgaccccc	atacttcttc	aaaggctgtg	gtaagttttg	cacagggtgag	180
ggcagcagaa	aggggggtant	tactgatgga	caccatcttc	tctgtatact	ccacactgac	240
cttgccatgg	gcaaaggccc	ctaccacaaa	aacaatagga	tactgctgg	gcaccagctc	300
acgcacatca	ctgacaaccg	ggatggaaaa	agaantgcc	actttcatac	atccaactgg	360
aaagtgatct	gatactggat	tcttaattac	cttcaaaagc	ttctgggggc	catcagctgc	420
tcgaacactg	a					431

<210> 170

<211> 266

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (266)

<223> n = A,T,C or G

<400> 170

acctgtgggc	tgggctgtta	tgcctgtgcc	ggctgctgaa	agggagtcca	gaggtggagc	60
tcaaggagct	ctgcaggcat	tttgccaanc	ctctccanag	canagggagc	aacctacact	120
ccccgctaga	aagacaccag	attggagtcc	tgggaggggg	agttgggggtg	ggcattttgat	180

gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240
tcaaagctag gggctctggca ggtgga 266

<210> 171
<211> 1248
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(1248)
<223> n = A,T,C or G

<400> 171
ggcagccaaa tcataaacgg cgaggactgc agcccgcaact cgcagccctg gcaggcgga 60
ctggatcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcattccgca gtgggtgctg 120
tcagccgcac actgtttcca gaagtgaagt gagagctcct acaccatcgg gctgggcctg 180
cacagtcttg aggcgacca agagccaggg agccagatgg tggaggccag cctctccgta 240
cggcaccag agtacaacag acccttgctc gctaaccgacc tcatgctcat caagtggac 300
gaatccgtgt ccgagctga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360
gcggggaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420
gtgctgcagt gcgtgaacgt gtcgggtggtg tctgaggagg tctgcagtaa gctctatgac 480
ccgctgtacc accccagcat gttctgcgcc ggcggaggggc aagaccagaa ggactcctgc 540
aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtctttc 600
ggaaaagccc cgtgtggcca agttggcgtg ccagggtgtct acaccaacct ctgcaaattc 660
actgagtggg tagagaaaac cgtccaggcc agttaactct ggggactggg aacccatgaa 720
attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agccccctct 780
ccctcaggcc caggagtcca ggcgccagc ccctcctccc tcaaaccaag ggtacagatc 840
cccagcccct cctccctcag acccaggagt ccagaccccc cagccccctc tccctcagac 900
ccaggagtcc agcccctcct ccctcagacc caggagtcca gacccccag ccctcctcc 960
ctcagaccca ggggtccagg cccccaaccc ctccctccctc agactcagag gtccaagccc 1020
ccaaccntc attccccaga cccagaggtc caggtcccag ccctctntcc ctcagaccca 1080
gcggtccaat gccacctaga ctntccctgt acacagtgcc cccttggtggc acgttgaccc 1140
aaccttacca gttggtttt catttttngt ccctttcccc tagatccaga aataaagttt 1200
aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1248

<210> 172
<211> 159
<212> PRT
<213> Homo sapien

<220>
<221> VARIANT
<222> (1)...(159)
<223> Xaa = Any Amino Acid

<400> 172
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
1 5 10 15
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
20 25 30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
35 40 45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
50 55 60


```

Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
65              70              75              80
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
              85              90              95
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
              100             105             110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
              115             120             125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
              130             135             140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
145              150              155

```

<210> 173

<211> 1265

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1265)

<223> n = A,T,C or G

<400> 173

```

ggcagcccg c actcgcagcc ctggcagggc gcactgggtca tggaaaacga attgttctgc      60
tcgggcgctc tgggtgcatcc gcagtgggtg ctgtcagccg cacactgttt ccagaactcc      120
tacaccatcg ggctgggcct gcacagtctt gagggccgacc aagagccagg gagccagatg      180
gtggaggcca gcctctccgt acggcaccca gagtacaaca gacccttgct cgctaacgac      240
ctcatgctca tcaagttgga cgaatccgtg tccgagtcgt acaccatccg gagcatcagc      300
attgcttcgc agtgccctac cgcggggaac tcttgccctg tttctggctg gggctctgctg      360
gcgaacgggt agctcacggg tgtgtgtctg ccctcttcaa ggaggtcctc tgcccagtcg      420
cgggggctga ccagagctc tgcgtcccag gcagaatgcc taccgtgctg cagtgcgtga      480
acgtgtcggt ggtgtctgag gaggtctgca gtaagctcta tgaccgctg taccaccca      540
gcatgttctg cgccggcgga gggcaagacc agaaggactc ctgcaacggg gactctgggg      600
ggcccctgat ctgcaacggg tacttgacgg gccttggtgc tttcggaaaa gcccgtgtg      660
gccaagttgg cgtgccagg gtctacacca acctctgcaa attcactgag tggatagaga      720
aaaccgtcca ggccagttaa ctctggggac tgggaaccca tgaaattgac ccccaaatac      780
atcctgcgga aggaattcag gaatatctgt tcccagcccc tcctccctca ggcccaggag      840
tccaggcccc cagccccctc tcctcaaac caagggtaca gatccccagc ccctcctccc      900
tcagaccagc gagtcagac cccccagccc ctctccctc agaccagga gtccagcccc      960
tcctcctca gaccagggag tccagacccc ccagcccctc ctccctcaga cccaggggtt     1020
gaggccccca acccctcctc cttcagagtc agaggtccaa gcccccaacc cctcggtccc     1080
cagacccaga ggtnnaggtc ccagcccctc ttcctcaga cccagnggtc caatgccacc     1140
tagattttcc ctgnacacag tgcccccttg tggngngttg acccaacctt accagttggg     1200
ttttcatttt tngtcccttt ccctagatc cagaaataaa gtttaagaga nngcaaaaa     1260
aaaaa                                           1265

```

<210> 174

<211> 1459

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1459)

<223> n = A,T,C or G

<400> 174

gggcagccgc	acactgtttc	cagaagttag	tgcagagctc	ctacaccatc	gggctgggccc	60
tgcacagtct	tgaggccgac	caagagccag	ggagccagat	gggtggaggcc	agcctctccg	120
tacggcacc	agagtacaac	agacccttgc	tcgctaacga	cctcatgctc	atcaagttag	180
acgaatccgt	gtccgagtct	gacaccatcc	ggagcatcag	cattgcttcg	cagtgcctta	240
ccgcggggaa	ctcttgccctc	gtttctggct	ggggtctgct	ggcgaacggg	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggtcct	ctgcccagtc	gcgggggctg	acccagagct	360
ctgctgcccc	ggcagaatgc	ctaccgtgct	gcagtgcgtg	aacgtgtcgg	tggtgtctga	420
ngaggtctgc	antaagctct	atgaccgct	gtaccacccc	ancatgttct	gcgccggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcaggcgact	540
caggggaagg	tggagaagg	ggagacagag	acacacaggg	ccgcatggcg	agatgcagag	600
atggagagac	acacagggag	acagtgacaa	ctagagagag	aaactgagag	aaacagagaa	660
ataaacacag	gaataaagag	aagcaaaagg	agagagaaac	agaaacagac	atggggaggc	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcatggggcc	tgaggggcgg	780
gacctccacc	caatagaaaa	tcctcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtgcattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttga	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	ttttttaaat	tgttgcaact	ctcctaaaat	ttttctgatg	tgtttattga	1020
aaaaatccaa	gtataagtgg	acttgtgcat	tcaaaccagg	gttggttcaag	ggtcaactgt	1080
gtaccagag	ggaaacagtg	acacagattc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aatcaagac	tctacaaaga	ggctgggcag	gggtggctcat	gcctgtaatc	ccagcattt	1200
gggaggcgag	gcaggcgagat	cacttgaggt	aaggagttca	agaccagcct	ggccaaaatg	1260
gtgaaatcct	gtctgtacta	aaaatacaaa	agttagctgg	atatggtggc	aggcgcctgt	1320
aatcccagct	acttgggagg	ctgaggcgag	agaattgctt	gaatatggga	ggcagaggtt	1380
gaagtgaagt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaaa					1459

<210> 175

<211> 1167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (1167)

<223> n = A,T,C or G

<400> 175

gcgcagccct	ggcaggcggc	actggctcatg	gaaaaacgaat	tgttctgctc	gggcgtcctg	60
gtgcattccg	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggg	120
ctgggctctg	acagtcttga	ggccgaccaa	gagccaggga	gccagatggg	ggaggccagc	180
ctctccgtac	ggcaccaga	gtacaacaga	ctcttgctcg	ctaacgacct	catgctcatc	240
aagttggacg	aatccgtgtc	cgagtctgac	accatccgga	gcatcagcat	tgttctgcag	300
tgcctaccg	cggggaactc	ttgcctcgtn	tctggctggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgctgcaactg	cgtgaacgtg	tcggtgggtg	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgccg	gcggaggggc	agaccagaag	480
gactcctgca	acggtgactc	tggggggccc	ctgatctgca	acgggtactt	gcagggcctt	540
gtgtctttcg	gaaaagcccc	gtgtggccaa	cttggcgtgc	caggtgtcta	caccaacctc	600
tgcaaatcca	ctgagtggat	agagaaaacc	gtccagncca	gttaactctg	gggactggga	660
acccatgaaa	ttgaccccc	aatacatcct	gcggaangaa	ttcaggaata	tctgttccca	720
gccccctctc	cctcaggccc	aggagtccag	gccccagccc	cctcctccct	caaaccaagg	780
gtacagatcc	ccagccccctc	ctccctcaga	cccaggagtc	cagaccccc	agccccctnt	840
ccntcagacc	caggagtcca	gccccctctc	cntcagacgc	aggagtccag	acccccagc	900

```

ccntcntccg tcagacccag ggggtgcaggc ccccaacccc tcntccntca gagtcagagg      960
tccaagcccc caacccctcg ttccccagac ccagaggtnc aggtcccagc cctcctccc      1020
tcagacccag cgggtccaatg ccacctagan tntccctgta cacagtggcc ccttggtggca      1080
ngttgaccca acctaccag ttgggttttc attttttgtc cctttcccct agatccagaa      1140
ataaagtnta agagaagcgc aaaaaaa      1167

```

```

<210> 176
<211> 205
<212> PRT
<213> Homo sapien

```

```

<220>
<221> VARIANT
<222> (1) ... (205)
<223> Xaa = Any Amino Acid

```

```

<400> 176
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1      5      10      15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20      25      30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35      40      45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
 50      55      60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65      70      75      80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85      90      95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
 100     105     110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
 115     120     125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
 130     135     140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
 145     150     155     160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
 165     170     175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
 180     185     190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
 195     200     205

```

```

<210> 177
<211> 1119
<212> DNA
<213> Homo sapien

```

```

<400> 177
gcgcactcgc agccctggca ggcggcactg gtcattggaaa acgaattggt ctgctcgggc      60
gtcctggtgc atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctctacacc      120
atcgggctgg gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag      180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg      240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct      300

```

```

tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctgggggtct gctggcggaac 360
gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc 420
caaccctggc aggggtgtac catttcggca acttccagtg caaggacgtc ctgctgcatc 480
ctcactgggt gctcactact gctcactgca tcacccgga cactgtgata aactagccag 540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660
cagttatcct cactgaattg agatttcctg cttcagtgct agccattccc acataatttc 720
tgacctacag aggtgaggga tcatatagct cttcaaggat gctgggtactc ccctcacaaa 780
ttcatttctc ctgttgtagt gaaagggtgcg ccctctggag cctcccaggg tgggtgtgca 840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg 900
ctcagtacac cagggcaggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca 960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg 1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc 1080
ttaataaaca gaagctgtga tgtaaaaaa aaaaaaaaaa 1119

```

<210> 178

<211> 164

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(164)

<223> Xaa = Any Amino Acid

<400> 178

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1          5          10          15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
100          105          110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
115          120          125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
130          135          140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145          150          155          160
Pro Gly Thr Leu

```

<210> 179

<211> 250

<212> DNA

<213> Homo sapien

<400> 179

```

ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct    60
ccagctgccc cgggccgggg gatgcgaggc tcggagcacc cttgcccggc tgtgattgct    120
gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgctga    180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa    240
aaaaaaaaaa                                250

```

<210> 180

<211> 202

<212> DNA

<213> Homo sapien

<400> 180

```

actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca    60
tcaccagac ccgcccctg ccgctgcccc acgctgctgc taacgacagt atgatgctta    120
ctctgtact cggaaactat ttttatgtaa ttaatgtatg ctttcttgtt tataaatgcc    180
tgatttaaaa aaaaaaaaaa aa                                202

```

<210> 181

<211> 558

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(558)

<223> n = A,T,C or G

<400> 181

```

tccytgtgkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg    60
aatgtttagg cagtgttagt aatttcytcg taatgattct gttattactt tcctnattct    120
ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa    180
ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca    240
aaattatgca agttagtaat tactcagggg taactaaatt actttaatat gctggtgaac    300
ctactctgtt ccttggtctg aaaaaattat aaacaggact ttgttagttt gggaagccaa    360
attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw    420
ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt    480
aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc    540
caaaaaaaaa aaaaaaaaaa                                558

```

<210> 182

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(479)

<223> n = A,T,C or G

<400> 182

```

acagggttk grggatgcta agsccccrga rwtygtttga tccaaccctg gcttwttttc    60
agaggggaaa atggggccta gaagttacag mscatytagy tggcgcmgtg gcacccctgg    120
cstcacacag astcccagag agctgggact acaggcacac agtactgaa gcaggccctg    180
ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca    240
ctaagggttaa actttcccac ccagaaaagg caacttagat aaaatcttag agtactttca    300

```

tactmttcta agtcctcttc cagcctcact kkgagtcctm cytgggggtt gataggaant	360
ntctcttggc tttctcaata aartctctat ycatctcatg ttttaattgg tacgcatara	420
awtgstgara aaattaaaat gttctggtty macttttaaaa araaaaaaaa aaaaaaaaaa	479

<210> 183

<211> 384

<212> DNA

<213> Homo sapien

<400> 183

aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc	60
agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtggagg ctccagtgc	120
ggtgccagcc tgaccgccac tctcacattt gggctcttcg ctggccttgg tggagctggt	180
gccagcacca gtggcagctc tggcgctgtt ggtttctcct acaagtgaga ttttagatat	240
tgtaaatcct gccagtcttt ctcttcaagc cagggtgcat cctcagaaac ctactcaaca	300
cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt	360
gccatttcaa aaaaaaaaaa aaaa	384

<210> 184

<211> 496

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(496)

<223> n = A,T,C or G

<400> 184

accgaattgg gaccgctggc ttataagcga tcatgtyynt ccrgtatkac ctcaacgagc	60
agggagatcg agtctatacg ctgaagaaat ttgaccgat gggacaacag acctgctcag	120
cccatacctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga	180
aacgcttcaa ggtgctcatg acccagcaac cgcgcctgt cctctgaggg tcccttaaac	240
tgatgtcttt tctgccacct gttaccctc ggagactccg taaccaaact ctccggactg	300
tgagccctga tgcctttttg ccagccatac tctttggcat ccagtctctc gtggcgattg	360
attatgcttg tgtgaggcaa tcatggtggc atcacccata aagggaacac atttgacttt	420
tttttctcat attttaatt actacmagaw tattwmagaw waaatgawtt gaaaaactst	480
taaaaaaaaa aaaaaa	496

<210> 185

<211> 384

<212> DNA

<213> Homo sapien

<400> 185

gctggtagcc tatggcgkgg cccacggagg ggctcctgag gccacggrac agtgacttcc	60
caagtatcyt gcgcsgcgtc ttctaccgtc cctacctgca gatcttcggg cagattcccc	120
aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcggag cccggcttct	180
gggcacaccc tcttggggcc caggcgggca cctgcgtctc ccagtatgcc aactggcttg	240
tggtgctgct cctcgctcgc ttctgctcg tggccaacat cctgctggtc aacttgctca	300
ttgccatgtt cagttacaca ttccggcaag tacagggcaa cagcgatctc tactgggaag	360
gcgcagcgtt accgcctcat ccgg	384

<210> 186

<211> 577

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(577)

<223> n = A,T,C or G

<400> 186

gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cytcctggca	tcttggggcg	gcntaatatt	120
ccaggaaact	ctcaatcaag	tcaccgtcga	tgaaacctgt	gggctgggtc	tgtcttccgc	180
tcggtgtgaa	aggatctccc	agaaggagtg	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcga	ttctgcatgt	ccagcaggag	gttgtaccag	ctctctgaca	gtgaggtcac	300
cagccctatc	atgccgttga	mcgtgccgaa	garcaccgag	ccttgtgtgg	gggkkgaggt	360
ctcaccacga	ttctgcatta	ccagagagcc	gtggcaaaag	acattgacaa	actcggccag	420
gtggaaaaag	amcamctcct	ggargtgctn	gccgctcctc	gtcmgttggt	ggcagcgctw	480
tccttttgac	acacaaaaca	gttaaaggca	ttttcagccc	ccagaaantt	gtcatcatcc	540
aagatntcgc	acagcactna	tccagttggg	attaaat			577

<210> 187

<211> 534

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(534)

<223> n = A,T,C or G

<400> 187

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgstg	agaatycatw	60
actkggaaaa	gmaacattaa	agcctggaca	ctgggtattaa	aattcacaat	atgcaacact	120
ttaaacagtg	tgtcaatctg	ctcccyynac	tttgtcatca	ccagtctggg	aakaagggtta	180
tgccctattc	acacctgtta	aaagggcgct	aagcattttt	gattcaacat	cttttttttt	240
gacacaagtc	cgaaaaaagc	aaaagtaaac	agttatyaat	ttgttagcca	attcactttc	300
ttcatgggac	agagccatyt	gatttaaaaa	gcaaattgca	taatattgag	cttygggagc	360
tgatatttga	gcggaagagt	agcctttcta	cttcaccaga	cacaactccc	tttcatattg	420
ggatgttnac	naaagtwatg	tctctwacag	atgggatgct	tttgtggcaa	ttctgttctg	480
aggatctccc	agtttattta	ccacttgcac	aagaaggcgt	tttcttcctc	aggc	534

<210> 188

<211> 761

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(761)

<223> n = A,T,C or G

<400> 188

agaaaccagt	atctctnaaa	acaacctctc	ataccttggtg	gacctaat	ttgtgtgcgtg	60
ttgtgtgtgcg	cgcataattat	atagacaggc	acatcttttt	tacttttgta	aaagcttatg	120
cctctttggg	atctatatct	gtgaaagttt	taatgatctg	ccataatgtc	ttggggacct	180

```

ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt      240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc ctkgackarg      300
ggggacaaag aaaagcaaaa ctgamcataa raacaatwa cctggtgaga arttgcataa      360
acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtktt wttctccctt      420
gcaaaaaaca tgtacngact tcccgttgag taatgccaaag ttgttttttt tatnataaaa      480
cttgccttcc attacatggt tnaaagtggg gtggtggggc aaaatattga aatgatggaa      540
ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac      600
atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta      660
tttttctgtt ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac      720
gaaaataata acattgaaga aaaaananaa aaanaaaaaa a                                     761

```

<210> 189

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (482)

<223> n = A,T,C or G

<400> 189

```

tttttttttt ttgtccgatn ctactatttt attgcaggan gtgggggtgt atgcaccgca      60
caccgggggt atnagaagca agaaggaaag agggagggca cagccccttg ctgagcaaca      120
aagccgcctg ctgccttctc tgtctgtctc ctggtgcagg cacatgggga gaccttcccc      180
aaggcagggg ccaccagtcc aggggtggga atacaggggg tgggangtgt gcataagaag      240
tgataggcac aggccacccg gtacagaccc ctccggtctc gacaggtnga ttctgaccag      300
gtcattgtgc cctgcccagg cacagcgtan atctggaaaa gacagaatgc ttcccttttc      360
aaatttggct ngtcatngaa ngggcanttt tccaanttng gctnngtctt ggtaacnctg      420
gttcggccca gctccncgtc caaaaantat tcaccnctt ccnaattgct tgcnggnccc      480
cc                                     482

```

<210> 190

<211> 471

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (471)

<223> n = A,T,C or G

<400> 190

```

tttttttttt ttttaaaaca gtttttcaca acaaaattta ttagaagaat agtgggtttg      60
aaaactctcg catccagtga gaactaccat acaccacatt acagctngga atgtntcca      120
aatgtctggg caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag      180
cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt      240
taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt      300
tgaaaaattt catgtatgca atccaacca agaacttnat tgggtgatcat gantnctcta      360
ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacnngt acaaaaaanaa      420
tctgtaattn anttcaacct ccgtacngaa aaatnttntt tatacactcc c                                     471

```

<210> 191

<211> 402

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (402)

<223> n = A,T,C or G

<400> 191

gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct	60
gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa	120
attcttcacc agtcacatct tctaggacct ttttggattc agttagtata agctcttcca	180
cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaagg aattyaattg	240
ctcgttctct aacaatgtcc tctccttgaa gtattttggc gaacaaccca cctaaagtcc	300
ctttgtgcat ccattttaaa tatacttaat agggcattgk tncactaggt taaattctgc	360
aagagtcac tgtctgcaaa agttgcgtta gtatatctgc ca	402

<210> 192

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (601)

<223> n = A,T,C or G

<400> 192

gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnnaact	60
ggtctacccc acatgggagc agcatgccgt agntatataa ggctattccc tgagtcagac	120
atgcytyttt gaytaccgtg tgccaagtgc tgggtattct yaacacacyt ccattccggt	180
cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcaccc	240
acgagacact tgaagagggt aacaaagcga ytcttgcat gctttttgtc cctccggcac	300
cagttgtcaa tactaaccgc ctggtttgcc tccatcacat ttgtgatctg tagctctgga	360
tacatctcct gacagtactg aagaacttct tcttttgttt caaaagcarg tcttggtgcc	420
tgttggtatc gggtcccatt tcccagtcyg aatgttcaca tggcatattt wacttccac	480
aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag	540
cctcgatgta gccggccagc gccaaaggcag gcgccgtgag cccaccagc agcagaagca	600
g	601

<210> 193

<211> 608

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (608)

<223> n = A,T,C or G

<400> 193

atacagccca natcccacca cgaagatgcg ctgtgtgact gagaacctga tgcggtcact	60
ggtcccgtct tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcytt	120
cccaacgcag gcagmagcgg gscgggtcaa tgaactccay tcgtggcttg gggtkgacgg	180
tkaagtgcag gaagaggctg accacctcgc ggtccaccag gatgcccagc tgtgcgggac	240
ctgcagcgaa actcctcgat ggtcatgagc gggaagcgaa tgaggcccag ggccttgccc	300

```

agaaccttcc gcctgttctc tggcgtcacc tgcagctgct gccgctgaca ctgggcctcg      360
gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgcccagtg tgtcgcgctc      420
caggammgsc accagcgtgt ccagggtcaat gtcgggtgaag ccctccgagg gtrtgggcgt      480
ctgcagtggt tttgtcgatg ttctccaggc acaggctggc cagctgcggg tcatcgaaga      540
gtcgcgcctg cgtgagcagc atgaaggcgt tgtcggcctg cagttcttct tcaggaactc      600
cacgcaat                                         608

```

<210> 194

<211> 392

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 194

```

gaacggctgg accttgccct gcattgtgct tgcctggcagg gaataccttg gcaagcagyt      60
ccagtcggag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggccttcccc      120
tccgcctcaa tgcagaacca gtatggggag cactgtgttt agagttaaga gtgaacactg      180
tttgatttta cttgggaatt tctctgttta tatagctttt ccaatgcta atttccaaac      240
aacaacaaca aaataacatg tttgcctgtt aagttgtata aaagtaggtg attctgtatt      300
taaagaaaat attactgtta catatactgc ttgcaatttc tgtatttatt gktnctstgg      360
aaataaatat agttattaaa ggttgtcant cc                                         392

```

<210> 195

<211> 502

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(502)

<223> n = A,T,C or G

<400> 195

```

ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg      60
ccgagctgag gcagatgttc ccacagtgac cccagagacc stgggstata gtytctgacc      120
cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc      180
aaggggaagg cccattccgg ggstgttccc cgaggaggaa ggggaagggc tctgtgtgcc      240
ccccasgagg aagaggccct gagtcctggg atcagacacc ccttcacgtg tatccccaca      300
caaatgcaag ctcaccaagg tccccctctc gtcccccttc stacacctg amcggccact      360
gscscacacc caccagagc acgccaccgc ccatggggar tgtgctcaag gartcgcnng      420
gcarcgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt      480
gctnanaaaa aaaaanaaaa aa                                         502

```

<210> 196

<211> 665

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(665)

<223> n = A,T,C or G

<400> 196

```
ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc      60
cctctggaag ccttgcgagc agcggacttt gtaattgttg gagaataact gctgaatttt      120
wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga      180
actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkac      240
aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt      300
attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact      360
tcacttgggt attttattgt aaatgarta caaaattctt aatttaagar aatgggatgt      420
watatttatt tcattaattt ctttcctkgt ttacgtwaat ttgaaaaga wtgcatgatt      480
tcttgacaga aatcgatctt gatgctgtgg aagtagtttg acccacatcc ctatgagttt      540
ttcttagaat gtataaagg ttagagcccat cnaacttcaa agaaaaaat gaccacatac      600
tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan      660
aagtg                                           665
```

<210> 197

<211> 492

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(492)

<223> n = A,T,C or G

<400> 197

```
tttntttttt ttttttttgc aggaaggatt ccatttattg tggatgcatt ttcacaatat      60
atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg      120
aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtaaa gatnacagag      180
aattatagtc naaccagtaa acnaggaatt tacttttcaa aagattaaat ccaaactgaa      240
caaaattcta cctgaaact tactccatcc aaatattgga ataanagtca gcagtgtac      300
attctcttct gaactttaga ttttctagaa aaatagttaa tagtgatcag gaagagctct      360
tgttcaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc      420
catttcactc ccatacggg agtcaatgct acctgggaca cttgtatttt gttcatnctg      480
ancntggctt aa                                           492
```

<210> 198

<211> 478

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(478)

<223> n = A,T,C or G

<400> 198

```
tttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa      60
tgtntccacn acaaatcatn ttactnagtt aagaggccan ctacattgta caacatacac      120
tgagtatatt ttgaaaagga caagttaaaa gtanacncat attgccganc atancacatt      180
tatacatggc ttgattgata tttagcacag canaaaactga gtgagttacc agaaanaaat      240
natatatgtc aatcngatgt aagatacaaa acagatccta tggtagatan catcntgtag      300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaaga gatggccgta      360
agcattctag tacctctact ccatgggtta gaatcgtaca cttatgttta catatgtnc      420
```

gggtaagaat tgtgttaagt naanttatgg agagggtccan gagaaaaatt tgatncaa 478

<210> 199
 <211> 482
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(482)
 <223> n = A,T,C or G

<400> 199
 agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcactgaca atcagaccta 60
 tgctagttcc tgtcatctat tcgctactaa atgcagactg gaggggacca aaaaggggca 120
 tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga 180
 agtgattcag ttctctctac ggatgagaga ctgggtcaag aatatactca tgcagcttta 240
 tgaagccnac tctgaacacg ctgggtatct nagatgagaa ncagagaaat aaagtcnaga 300
 aaatttacct ggangaaaag aggccttngg ctggggacca tccattgaa ccttctctta 360
 anggacttta agaanaaact accacatgtn tgnngtatcc tgggtgcngg ccgtttantg 420
 aacntngacn ncacccttnt ggaatanant cttgacngcn tcctgaactt gctcctctgc 480
 ga 482

<210> 200
 <211> 270
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(270)
 <223> n = A,T,C or G

<400> 200
 cgcccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcc a gcagttggtc 60
 cgactgcgac gacggcgccg ggcacagtcg caggtgcagc gcgggcgcct ggggtcttgc 120
 aaggtcgagc tgacgccgca gaggtcgtgt cacgtccac gaccttgacg ccgtcgggga 180
 cagccggaac agagcccgtt gaangcggga ggcctcgggg agcccctcgg gaaggcgccg 240
 ccgagagata cgcaggtgca ggtggccgcc 270

<210> 201
 <211> 419
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(419)
 <223> n = A,T,C or G

<400> 201
 tttttttttt ttttgaatc tactgcgagc acagcaggtc agcaacaagt ttattttgca 60
 gctagcaagg taacagggtg gggcatggtt acatgttcag gtcaacttcc ttgtcgtgg 120
 ttgattgggt tgtctttatg ggggcggggg ggggtagggg aaancgaagc anaantaaca 180
 tggagtgggt gcaccctccc tgtagaacct ggttacnaaa gcttggggca gttcacctgg 240

tctgtgaccg	tcattttctt	gacatcaatg	ttattagaag	tcaggatata	ttttagagag	300
tccactgtnt	ctggaggag	attagggttt	cttgccaana	tccaancaaa	atccacntga	360
aaaagttgga	tgatncangt	acngaatacc	ganggcatan	ttctcatant	cgggtggcca	419

<210> 202

<211> 509

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (509)

<223> n = A,T,C or G

<400> 202

tttntttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
tggcacttaa	tccattttta	tttcaaaatg	tctacaaant	ttnaatncnc	cattatacng	120
gtnattttnc	aaaatctaaa	nnttattcaa	atntnagcca	aantccttac	ncaaatnnaa	180
tacnncnaaa	aatcaaaaat	atacntntct	ttcagcaaac	ttngttacat	aaattaaaaa	240
aatatatacg	gctgggtgtt	tcaaagtaca	attatcttaa	cactgcaaac	atnttttnaa	300
ggaactaaaa	taaaaaaaaa	cactnccgca	aaggttaaag	ggaacaacaa	attcntttta	360
caacancnnc	nattataaaa	atcatatctc	aaatcttagg	ggaatatata	cttcacacng	420
ggatcttaac	ttttactnca	ctttgtttat	ttttttanaa	ccattgtntt	gggccaaca	480
caatggnaat	nccnccnnc	tggaactagt				509

<210> 203

<211> 583

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (583)

<223> n = A,T,C or G

<400> 203

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaatggaaa	ctgccttaga	tacataatc	ttaggaatta	gcttaaaatc	tgccataaag	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
atttttcttg	tctttaaaat	tatctaactc	ttccattttt	tccctattcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaca	ggaagagana	atggcacaca	aaacaaacat	tttatattca	tatttctacc	420
tacgttaata	aaatagcatt	ttgtgaagcc	agctcaaaaag	aaggcttaga	tccttttatg	480
tccatttttag	tcactaaacg	atatchaaaag	tgccagaatg	caaaaagggtt	gtgaacattt	540
attcaaaagc	taatataaga	tatttcacat	actcatcttt	ctg		583

<210> 204

<211> 589

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (589)

<223> n = A,T,C or G

<400> 204

ttttttttnt tttttttttt ttttttnctc ttcttttttt ttganaatga ggatcgagtt	60
tttcactctc tagatagggc atgaagaaaa ctcatctttc cagctttaaa ataacaatca	120
aatctcttat gctatatcat attttaagtt aaactaatga gtcactggct tatcttctcc	180
tgaaggaaat ctgttcattc ttctcattca tatagttata tcaagtacta ccttgcatat	240
tgagaggttt ttcttctcta ttacacata tatttccatg tgaatttgta tcaaaccctt	300
attttcatgc aaactagaaa ataatgtntt cttttgcata agagaagaga acaatatnag	360
cattacaaaa ctgctcaaat tggttggtta gnttatccat tataattagt tnggcaggag	420
ctaatacaaa tcacatttac ngacnagcaa taataaaact gaagtaccag ttaaatatcc	480
aaaataatta aaggaacatt tttagcctgg gtataattag ctaattcact ttacaagcat	540
ttattnagaa tgaattcaca tggtattatt cntagccca acacaatgg	589

<210> 205

<211> 545

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(545)

<223> n = A,T,C or G

<400> 205

ttttntttt ttttttcagt aataatcaga acaatattta tttttatatt taaaattcat	60
agaaaagtgc cttacattta ataaaagttt gtttctcaaa gtgatcagag gaattagata	120
tngtcttgaa caccaatatt aatttgagga aaatacacca aaatacatta agtaaattat	180
ttaagatcat agagcttgta agtgaaaaga taaaatttga cctcagaaac tctgagcatt	240
aaaaatccac tattagcaaa taaattacta tggacttctt gctttaattt tgtgatgaat	300
atggggtgtc actggtaaac caacacattc tgaaggatac attacttagt gatagattct	360
tatgtacttt gctanatnac gtggatatga gttgacaagt ttctctttct tcaatctttt	420
aaggggcnaga ngaaatgagg aagaaaagaa aaggattacg catactgttc tttctatngg	480
aaggattaga tatgtttcct ttgccaatat taaaaaata ataatgttta ctactagtga	540
aaccc	545

<210> 206

<211> 487

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(487)

<223> n = A,T,C or G

<400> 206

ttttttttt ttttttagtc aagtttctna tttttattat aattaaagtc ttggtcattt	60
catttattag ctctgcaact tacatattta aattaaagaa acgttnttag acaactgtna	120
caatttataa atgtaagggtg ccattattga gtanatatat tctccaaga gtggatgtgt	180
cccttctccc accaactaat gaancagcaa cattagttta attttattag tagatnatac	240
actgtgcaa acgctaattc tcttctccat ccccatgtng atattgtgta tatgtgtgag	300
ttggtnagaa tgcatacanca atctnacaat caacagcaag atgaagctag gcntgggctt	360
tgggtgaaaa tagactgtgt ctgtctgaat caaatgatct gacctatcct cgggtggcaag	420
aactcttcga accgcttctt caaaggcngc tgccacattt gtggcntctn ttgcacttgt	480

ttcaaaa

487

<210> 207

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 207

tgaattggct	aaaagactgc	atTTTTanaa	ctagcaactc	ttatttcttt	cctttaaaaa	60
tacatagcat	taaatcccaa	atcctattta	aagacctgac	agcttgagaa	ggtcactact	120
gcatttatag	gaccttctgg	tggttctgct	gttacntttg	aantctgaca	atccttgana	180
atctttgcat	gcagaggagg	taaaaggat	tggaatttca	cagaggaana	acacagcgca	240
gaaatgaagg	ggccaggctt	actgagcttg	tccactggag	ggctcatggg	tgggacatgg	300
aaaagaaggc	agcctaggcc	ctggggagcc	ca			332

<210> 208

<211> 524

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(524)

<223> n = A,T,C or G

<400> 208

agggcggtgt	gcggaggcgc	ttactgtttt	gtctcagtaa	caataaatac	aaaaagactg	60
gttggtgtcc	ggcccatcc	aaccacgaag	ttgatttctc	ttgtgtgcag	agtgactgat	120
tttaaaggac	atggagcttg	tcacaatgtc	acaatgtcac	agtgtgaagg	gcacactcac	180
tcccgcgtga	ttcacattta	gcaaccaaca	atagctcatg	agtccatact	tgtaaatact	240
tttggcagaa	tacttnttga	aacttgcaga	tgataactaa	gatccaagat	atttcccaa	300
gtaaatagaa	gtgggtcata	atattaatta	cctgttcaca	tcagcttcca	tttacaagtc	360
atgagcccag	acactgacat	caaactaagc	ccacttagac	tcctcaccac	cagtctgtcc	420
tgtcatcaga	caggaggctg	tcaccttgac	caaattctca	ccagtcaatc	atctatccaa	480
aaaccattac	ctgatccact	tccggtaatg	caccaccttg	gtga		524

<210> 209

<211> 159

<212> DNA

<213> Homo sapien

<400> 209

gggtgaggaa	atccagagtt	gccatggaga	aaattccagt	gtcagcattc	ttgctccttg	60
tggccctctc	ctacactctg	gccagagata	ccacagtcaa	acctggagcc	aaaaaggaca	120
caaaggactc	tcgacccaaa	ctgccccaga	ccctctcca			159

<210> 210

<211> 256

<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(256)
<223> n = A,T,C or G

<400> 210
actccctggc agacaaaggc agaggagaga gctctgttag ttctgtgttg ttgaactgcc 60
actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta 120
tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat 180
ttgcaggggtg naaatgggan ggctggtttg ttanatgaac agggacatag gaggtaggca 240
ccaggatgct aaatca 256

<210> 211
<211> 264
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(264)
<223> n = A,T,C or G

<400> 211
acattgtttt tttgagataa agcattgaga gagctctcct taacgtgaca caatggaagg 60
actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120
atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gttaaggaga 180
ggggagatac attcngaaag aggactgaaa gaaataactca agtnggaaaa cagaaaaaga 240
aaaaaaggag caaatgagaa gcct 264

<210> 212
<211> 328
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 212
acccaaaaat ccaatgctga atatttggtc tcattattcc canattcttt gattgtcaaa 60
ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120
gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag 180
ttnaatttca ttcccatgga ctgggatcc ttatcatcag ccagagagat tgaaaattta 240
ccctacnac tctttactct ctgganaggg ccagtgggtg tagctataag cttggccaca 300
tttttttttc ctttattcct ttgtcaga 328

<210> 213
<211> 250
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature

<222> (1) ... (250)

<223> n = A,T,C or G

<400> 213

acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt	60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgcca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatata tctctnacct	240
tctcatcggc	250

<210> 214

<211> 444

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (444)

<223> n = A,T,C or G

<400> 214

accagaatc caatgctgaa tatttggtt cattattccc agattctttg attgtcaaag	60
gatttaattg tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg	120
tttatatatg cagcaacaat attcaagcgc gacaacaggt tattgaactt gcccggcagg	180
tgaatttcat tccattgac ttgggaccc tcatcagc canagagatt gaaaatttac	240
ccctacgact ctttactctc tggagagggc cagtgggtgt agctataagc ttggccacat	300
ttttttttcc tttattcctt tgtcagagat gcgattcatc catatgctan aaaccaacag	360
agtgactttt acaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt	420
actttgctct ccctaataata cctc	444

<210> 215

<211> 366

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (366)

<223> n = A,T,C or G

<400> 215

acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt	60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgcca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataagc catgttgaga aacaaatata tctctgacct	240
tctcatcggc aagcagaggc tgtaggcaac atggaccata gcgaanaaaa aacttagtaa	300
tccaagctgt tttctacact gtaaccaggc ttccaaccaa ggtggaaatc tcctatactt	360
ggtgcc	366

<210> 216

<211> 260

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(260)
 <223> n = A,T,C or G

<400> 216
 ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60
 caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat 120
 taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttnggctgga aaatttaaaa 180
 atcaaaaatt tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240
 aattcttcct tccctccttt 260

<210> 217
 <211> 262
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(262)
 <223> n = A,T,C or G

<400> 217
 acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60
 tcttgccctat aattttctat ttaataagg aaatagcaaa ttgggggtggg gggaatgtag 120
 ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180
 atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttaccta 240
 atatccttca tgcttgtaaa gt 262

<210> 218
 <211> 205
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(205)
 <223> n = A,T,C or G

<400> 218
 accaagggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca 60
 cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaaagactc 120
 aggcctcccc agttctactg acctttgtcc ttangtntna ngtccagggt tgctaggaaa 180
 anaaatcagc agacacaggt gtaaa 205

<210> 219
 <211> 114
 <212> DNA
 <213> Homo sapien

<400> 219
 tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gccccatcca 60
 accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220
 <211> 93

<212> DNA

<213> Homo sapien

<400> 220

actagccagc acaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta	60
aaataagcat ttagtgctca gtcctactg agt	93

<210> 221

<211> 167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(167)

<223> n = A,T,C or G

<400> 221

actangtgca ggtgcgcaca aatatttgtc gatattccct tcattcttga ttccatgagg	60
tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc	120
ccccactac cttccctgac gctccccana aatcacccaa cctctgt	167

<210> 222

<211> 351

<212> DNA

<213> Homo sapien

<400> 222

agggcggtgt gcgaggggcg gtactgacct cattagtagg aggatgcatt ctggcacccc	60
gttcttcacc tgtcccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa	120
atggttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa	180
ttttctcttt tatatttcta gaagaagtgt ctttgagcct attagatccc gggaatcttt	240
taggtgagca tgattagaga gcttgtagggt tgcttttaca tatatctggc atatttgagt	300
ctcgtatcaa aacaatagat tggtaaagggt ggtattattg tattgataag t	351

<210> 223

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 223

aaaacaaaca aacaaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat	60
tggttaattat ggtcaattta atwrtttkt ggggcatttc cttacattgt cttgacaaga	120
ttaaaatgtc tgtgccaaaa ttttgatatt tatttgagga cttcttatca aaagtaatgc	180
tgccaaagga agtctaagga attagtagtg ttcccmcac ttgtttgag tgtgctattc	240
taaaagattt tgatttcctg gaatgacaat tatattttaa ctttggtggg ggaaanagtt	300
ataggaccac agtcttcact tctgatactt gttaaattaat cttttattgc acttgttttg	360
accattaagc tatatgttta aaa	383

<210> 224

<211> 320
 <212> DNA
 <213> Homo sapien

<400> 224
 cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga 60
 aaaagtttgt gacattgttag tagggagtgt gtacccttta ctcccatca aaaaaaaat 120
 ggatacatgg ttaaaggata raagggaat atttatcat atgttctaaa agagaaggaa 180
 gagaaaatac tactttctcr aaatggaagc ccttaaagggt gctttgatac tgaaggacac 240
 aaatgtggcc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctgttgagcgt 300
 tttaractcm gcattgtgac 320

<210> 225
 <211> 1214
 <212> DNA
 <213> Homo sapien

<400> 225
 gaggactgca gcccgcactc gcagccctgg caggcgccac tggatcatgga aaacgaattg 60
 ttctgctcgg gcgtcctggg gcacccgcag tgggtgctgt cagccgcaca ctgtttccag 120
 aactcctaca ccacggggt gggcctgcac agtcttgagg ccgaccaaga gccagggagc 180
 cagatgggtgg aggccagcct ctccgtacgg caccagagt acaacagacc ctgtctcgt 240
 aacgacctca tgcctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 300
 atcagcattg cttcgcagtg ccctaccgcg ggggaactctt gcctcgtttc tggctggggg 360
 ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct 420
 gaggagggtct gcagtaagct ctatgacccg ctgtaccacc ccagcatgtt ctgcgccggc 480
 ggagggaag accagaagga ctctgcaac ggtgactctg gggggccctt gatctgcaac 540
 ggggtacttgc agggccttgt gtctttcga aaagcccggt gtggccaagt tggcgtgcca 600
 ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt 660
 taactctggg gactgggaac ccatagaatt gaccccaaa tacatcctgc ggaaggaatt 720
 caggaatatc tgttcccagc cctcctccc tcaggccag gagtccaggc cccagcccc 780
 tcctccctca aaccaagggt acagatcccc agccctcct cctcagacc caggagtcca 840
 gacccccag cccctcctcc ctccagacca ggagtccagc cctcctccc tcagaccag 900
 gagtccagac cccccagccc ctccctccc agaccagggt gtccaggccc ccaaccctc 960
 ctccctcaga ctccagaggt caagccccc accctcctt cccagaccc agagggtccag 1020
 gtcccagccc ctccctccc agaccagcg gtccaatgcc acctagactc tcctgttaca 1080
 cagtgcctcc ttgtggcag ttgacccaac cttaccagtt ggtttttcat tttttgtccc 1140
 tttcccttag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaaaaaaaa aaaa 1214

<210> 226
 <211> 119
 <212> DNA
 <213> Homo sapien

<400> 226
 acccagtatg tgcagggaga cggaacccca tgtgacagcc cactccacca gggttcccaa 60
 agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt 119

<210> 227
 <211> 818
 <212> DNA
 <213> Homo sapien

<400> 227

acaattcata	gggacgacca	atgaggacag	ggaatgaacc	cggctctccc	ccagccctga	60
tttttgctac	atatggggtc	ccttttcatt	ctttgcaaaa	acactggggt	ttctgagaac	120
acggacgggt	cttagcacia	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttcctc	ctctggagga	aaggtgggtga	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca	cgctcggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgctccc	ttccaatcag	ccacttctga	gaacccccat	ctaacttctc	actggaaaag	360
agggcctcct	caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaaggggtg	caccctcagc	agagaagccg	agagcttaac	tctggctcgt	tccagagaca	480
acctgctggc	tgtcttggga	tgcgccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggacatgaag	ctgaggacac	tgggcttcaa	cactgagttg	tcattgaggg	600
gacaggctct	gccctcaagc	cggctgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggct	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtcgtgt			818

<210> 228

<211> 744

<212> DNA

<213> Homo sapien

<400> 228

actggagaca	ctgttgaact	tgatcaagac	ccagaccacc	ccaggctctcc	ttcgtgggat	60
gtcatgacgt	ttgacatacc	tttggaaacga	gcctcctcct	tggaaagatgg	aagaccgtgt	120
tcgtggccga	cctggcctct	cctggcctgt	ttcttaagat	gcggagtcac	atttcaatgg	180
taggaaaagt	ggcttcgtaa	aatagaagag	cagtcactgt	ggaactacca	aatggcgaga	240
tgctcgggtgc	acattgggggt	gctttgggat	aaaagattta	tgagccaact	attctctggc	300
accagattct	aggccagttt	gttccactga	agcttttccc	acagcagtc	acctctgcag	360
gctggcagct	gaatggcttg	ccggtggctc	tgtggcaaga	tcacactgag	atcgatgggt	420
gagaaggcta	ggatgcttgt	ctagtgttct	tagctgtcac	gttggctcct	tccaggtttg	480
ccagacgggtg	ttggccactc	ccttctaaaa	cacaggcgcc	ctcctgggtga	cagtgaaccg	540
ccgtgggtatg	ccttggccca	ttccagcagt	cccagttatg	catttcaagt	ttggggtttg	600
ttcttttctg	taatgttctc	ctgtgttgtc	agctgtcttc	atttctggg	ctaagcagca	660
ttgggagatg	tggaccagag	atccactcct	taagaaccag	tggcgaaaga	cactttcttt	720
cttcactctg	aagtagctgg	tggt				744

<210> 229

<211> 300

<212> DNA

<213> Homo sapien

<400> 229

cgagtctggg	ttttgtctat	aaagtttgat	ccctcctttt	ctcatccaaa	tcattgtgaac	60
cattacacat	cgaataaaaa	gaaaggtggc	agacttgccc	aacgccaggc	tgacatgtgc	120
tgcagggttg	ttgtttttta	attattattg	ttagaaacgt	caccacagc	ccctgttaat	180
ttgtatgtga	cagccaactc	tgagaaggtc	ctatttttcc	acctgcagag	gatccagctc	240
cactaggctc	ctccttgccc	tcacactgga	gtctccgcca	gtgtgggtgc	ccactgacat	300

<210> 230

<211> 301

<212> DNA

<213> Homo sapien

<400> 230

cagcagaaca	aatacaata	tgaagagtgc	aaagatctca	taaaatctat	gctgaggaat	60
gagcgacagt	tcaaggagga	gaagcttgca	gagcagctca	agcaagctga	ggagctcagg	120

caatataaag tcttggttca cactcaggaa cgagagctga cccagttaag ggagaagttg 180
 cgggaaggga gagatgcctc cctctcattg aatgagcacc tccaggccct cctcactccg 240
 gatgaaccgg acaagtccca ggggcaggac ctccaagaaa cagacctcgg ccgcgaccac 300
 g 301

<210> 231

<211> 301

<212> DNA

<213> Homo sapien

<400> 231

gcaagcacgc tggcaaatct ctgtcaggtc agctccagag aagccattag tcatttttagc 60
 caggaactcc aagtccacat ccttggcaac tggggacttg cgcaggttag ccttgaggat 120
 ggcaacacgg gacttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg 180
 tctgaggatg gcaggatcaa tgatgtcagg ccggttggtg ccgccaatga tgaacacatt 240
 tttttttgtg gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc 300
 c 301

<210> 232

<211> 301

<212> DNA

<213> Homo sapien

<400> 232

agtaggtatt tctgtagaag ttcaacacca aaactggaac atagttctcc ttcaagtgtt 60
 ggcgacagcg gggttctctg attctggaat ataactttgt gtaaattaac agccacctat 120
 agaagagtc atctgctgtg aaggagagac agagaactct ggggtccgtc gtctgttcca 180
 cgtgctgtac caagtgtgtg tgccagcctg ttacctgttc tccactgaaa tctggctaatt 240
 gctctgtgt atcacttctg attctgacaa tcaatcaate aatggcctag agcactgact 300
 g 301

<210> 233

<211> 301

<212> DNA

<213> Homo sapien

<400> 233

atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggatttgag 60
 atgctaaggc cccagagatc gtttgatcca accctcttat ttccagaggg gaaaatgggg 120
 cctagaagtt acagagcacc tagctggtgc gctggcacc ctggcctcac acagactccc 180
 gagtagctgg gactacaggc acacagtcac tgaagcaggc cctggttagca attctatgcg 240
 taaaaattaa catgagatga gtagagactt tattgagaaa gcaagagaaa atcctatcaa 300
 c 301

<210> 234

<211> 301

<212> DNA

<213> Homo sapien

<400> 234

aggtcctaca catcgagact catccatgat tgatatgaat ttaaaaatta caagcaaaga 60
 cattttattc atcatgatgc tttcttttgt ttcttctttt cgttttcttc tttttctttt 120
 tcaatttcag caacatactt ctcaatttct tcaggattta aaatcttgag ggattgatct 180
 cgctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtgcc 240
 ttgatcacca gcttaatggt cagatcatct gcttcaatgg ctctgctcagt atagttcttc 300

t 301

<210> 235
 <211> 283
 <212> DNA
 <213> Homo sapien

<400> 235
 tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg 60
 aattccctca tcttttaggg aatcatttac caggtttgga gaggattcag acagctcagg 120
 tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata 180
 atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatatcaaca 240
 ttagggattc aaagaaatat tagatttaag ctcacactgg tca 283

<210> 236
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 236
 aggtcctcca ccaactgcct gaagcacggg taaaattggg aagaagtata gtgcagcata 60
 aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg 120
 tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggatatatag 180
 tgggtagacg gcttcatgag tacagtgtac tgtggatcgc taatctggac ttgggttgta 240
 aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc 300
 a 301

<210> 237
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 237
 cagtggtagt ggtgggtggac gtggcggttg tcgtgggtgcc ttttttggtg cccgtcacaa 60
 actcaatttt tggtcgctcc tttttggcct ttccaattt gtccatctca attttctggg 120
 ccttggctaa tgctcatag taggagtcct cagaccagcc atggggatca aacatattct 180
 ttgggtagtt ggtgccaaagc tcgtcaatgg cacagaatgg atcagcttct cgtaaattcta 240
 ggggtccgaa attctttctt cctttggata atgtagttca tatccattcc ctcttttatt 300
 t 301

<210> 238
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 238
 gggcagggtt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt 60
 gttcacagtt cagccccctg ctcaaaaaac caacgggccca gctaaggaga ggaggaggca 120
 ccttgagact tccggagtcg aggtctctca gggttcccca gccatcaat cattttctgc 180
 accccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca 240
 gtgtgggacc caggggtctg tcttcacagt aggaggtgga agggatgact aatttcttta 300
 t 301

<210> 239
 <211> 239

<212> DNA

<213> Homo sapien

<400> 239

ataagcagct agggaattct ttatttagta atgtcctaac ataaaagttc acataactgc	60
ttctgtcaaa ccatgatact gagctttgtg acaaccaga aataactaag agaaggcaaa	120
cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac	180
attcagccag tgagtagagt gtgaatgcc aacatacacag tatacaggtc cttcaggga	239

<210> 240

<211> 300

<212> DNA

<213> Homo sapien

<400> 240

ggtcctaag aagcagcagc ttccacattt taacgcagggt ttacgggtgat actgtccttt	60
gggatctgcc ctccagtga accttttaag gaagaagtgg gcccaagcta agttccacat	120
gctgggtgag ccagatgact tctgttccct ggtcacttcc ttcaatgggg cgaatggggg	180
ctgccagggt tttaaaatca tgcttcatct tgaagcacac ggtcacttca cctcctcac	240
gctgtgggtg tactttgatg aaaataccca ctttgttggc ctttctgaag ctataatgtc	300

<210> 241

<211> 301

<212> DNA

<213> Homo sapien

<400> 241

gaggtctggt gctgaggtct ctgggctagg aagaggaggt ctgtggagct ggaagccaga	60
cctcttttga ggaaactcca gcagctatgt tgggtgtctct gagggaaatgc aacaaggctg	120
ctcctccatg tattggaaaa ctgcaaaactg gactcaactg gaaggaaagt ctgctgccag	180
tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct	240
tctcctcct gtcatacagg ctctctcaag catcctttgt tgtcaggggc ctaaaaggga	300
g	301

<210> 242

<211> 301

<212> DNA

<213> Homo sapien

<400> 242

ccgaggtcct gggatgcaac caatcactct gtttcacgtg acttttatca ccatacaatt	60
tgtggcattt cctcattttc tacattgtag aatcaagagt gtaataaat gtatatcgat	120
gtcttcaaga atatatcatt cctttttcac tagaaccat tcaaaatata agtcaagaat	180
cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta	240
taagtacca aagttttata aatcaaaagc cctaattgata accattttta gaattcaatc	300
a	301

<210> 243

<211> 301

<212> DNA

<213> Homo sapien

<400> 243

aggtaagtcc cagtttgaag ctcaaaagat ctggtatgag cataggctca tcgacgacat	60
ggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg	120

tgacgtgcag tcggactctg tggcccaagg gstatggctct ctcggcatga tgaccagcgt 180
 gctggtttgt ccagatggca agacagtaga agcagaggct gcccacggga ctgtaacccg 240
 tcactaccgc atgttccaga aaggacagga gacgtccacc aatcccattg cttccatttt 300
 t 301

<210> 244

<211> 300

<212> DNA

<213> Homo sapien

<400> 244

gctggtttgc aagaatgaaa tgaatgattc tacagctagg acttaacctt gaaatggaaa 60
 gtcacgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc 120
 ccagggacct tggaaacagt tgacactgta aggtgcttgc tccccaaagac acatcctaaa 180
 aggtggtgta atggtgaaaa cgtcttcctt ctttattgcc ctttcttatt tatgtgaaca 240
 actggttgc ttttgtgtat cttttttaaa ctgtaaagtt caattgtgaa aatgaatc 300

<210> 245

<211> 301

<212> DNA

<213> Homo sapien

<400> 245

gtctgagtat taaaatgtt attgaaatta tccccacca atgttagaaa agaaagaggt 60
 tatatactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt 120
 aaggccagga gatattgtca ttaatgtara cttcaggaca ctagagtata gcagccctat 180
 gttttcaaag agcagagatg caattaaata ttgttttagca tcaaaaaggc cactcaatac 240
 agctaataaa atgaaagacc taatttctaa agcaattctt tataatttac aaagttttaa 300
 g 301

<210> 246

<211> 301

<212> DNA

<213> Homo sapien

<400> 246

ggtctgtcct acaatgcctg cttcttgaaa gaagtcggca ctttctagaa tagctaaata 60
 acctgggctt attttaaaga actatttgta gtcagattg gttttcctat ggctaaaata 120
 agtgcttctt gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac 180
 taacaatcat actaaatata ttttgaagta caaagtttga catgctctaa agtgacaacc 240
 caaatgtgtc ttacaaaaca cgttcctaac aaggtatgct ttacactacc aatgcagaaa 300
 c 301

<210> 247

<211> 301

<212> DNA

<213> Homo sapien

<400> 247

aggctcctttg gcagggtcctca tggatcagag ctcaaactgg agggaaaggc atttcgggta 60
 gcctaagagg gcgactggcg gcagcacaac caaggaaggc aaggttggtt cccccacgct 120
 gtgtcctgtg ttcaggtgcg acacacaatc ctcatgggaa caggatcacc catgctgtgc 180
 ccttgatgat caaggttggg gcttaagtgg attaaggag gcaagttctg ggttccttgc 240
 cttttcaaac catgaagtca ggctctgtat ccctcctttt cctaactgat attctaacta 300
 a 301

<210> 248
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 248
 aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact 60
 attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttaagaatt 120
 acaggaagaa agtggtttgg aagacagcca aagaaataaa agcagattaa attgtatcag 180
 gtacattcca gcctgttggc aactccataa aaacatttca gattttaatc ccgaatttag 240
 ctaatgagac tggatttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300
 c 301

<210> 249
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 249
 gtccagagga agcacctggt gctgaactag gcttgccctg ctgtgaactt gcacttggag 60
 ccttgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccgcgc 120
 ccagggagac acagcagtga ctcagagctg gtcgcacact gtgcctccct cctcaccgcc 180
 catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag 240
 actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt 300
 a 301

<210> 250
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 250
 ggtctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc 60
 cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc 120
 cataagcaca tcagtacttt tctctggctg gaatagtaaa cttaaagtatg gtacatctac 180
 ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240
 caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300
 a 301

<210> 251
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 251
 gccgaggtcc tacatttggc ccagtttccc cctgcatect ctccagggcc cctgcctcat 60
 agacaacctc atagagcata ggagaactgg ttgccctggg ggcaggggga ctgtctggat 120
 ggcaggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180
 cattgggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccgga 240
 cctctggagg ggggcagtgg aatcccagct ccaggacgga tcctgtcgaa aagatatcct 300
 c 301

<210> 252
 <211> 301

<212> DNA

<213> Homo sapien

<400> 252

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gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttctca      60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata      120
tcatttccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa      180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag taccctaaagt      240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc      300
a

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<210> 253

<211> 301

<212> DNA

<213> Homo sapien

<400> 253

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ttccctaaga agatgttatt ttgttgggtt ttgttccccc tccatctcga ttctcgtacc      60
caactaaaaa aaaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctcccttagct      120
tggtctgatt gttttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg      180
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt      240
tccatagtgc ccacagggtg ttcctcacat tttctccata ggaaaatgct ttttccaag      300
g

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<210> 254

<211> 301

<212> DNA

<213> Homo sapien

<400> 254

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cgctgcgcct ttcccttggg ggaggggcaa ggccagaggg ggtccaagtg cagcacgagg      60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc      120
ccaaatctct tcattctacc ctggtggact cctgactgta gaattttttg gttgaaacaa      180
gaaaaaataa aagcttttga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc      240
acttaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc      300
t

```

<210> 255

<211> 302

<212> DNA

<213> Homo sapien

<400> 255

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agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtc tttattataa      60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat      120
tgggattttg ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg      180
aggaaaaagg actggaggtg gaatctttat aaaaaacaag agtgattgag gcagattgta      240
aacattatta aaaaaacaaga aacaacaaca aaaaatagaga aaaaaaccac cccaacacac      300
aa

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<210> 256

<211> 301

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 256
 gttccagaaa acattgaagg tggttccca aagtctaact agggataccc cctctagcct 60
 aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc 120
 acccccacaaa gcctggacac cttgagcaca cagttatgac caggacagac tcctctctat 180
 aggcaaatac ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt 240
 gtggcctctc ggcctgggta gcaagaacat tcagggtagg cctaagttaa tcgtgttagt 300
 t 301

<210> 257
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 257
 gttgtggagg aactctggct tgctcattaa gtccactga ttttcactat cccctgaatt 60
 tccccactta tttttgtctt tcactatcgc aggccttaga agaggtctac ctgcctccag 120
 tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat 180
 gtcacattac tcccttcagt gatttcttgt agaagtgcc atccctgaat gccaccaaga 240
 tcttaattct cactcttcta atcttatctc tttgactcct ctttacaccg gagaaggctc 300
 c 301

<210> 258
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 258
 cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc 60
 agggggccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc 120
 ccaggggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg 180
 atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat 240
 tgggtgatccc tgggagcgcc ggtggagtaa cgttgggtcca tggaaagcag cgccacaac 300
 t 301

<210> 259
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 259

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tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg      60
gtgtcctgaa gtgatttgga cccctgaggg cagacaccta agtaggaatc ccagtgggaa      120
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtggggccag gaaggctctgt      180
tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggctt      240
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcataccttg ctccaggtgg      300
c

```

```

<210> 260
<211> 301
<212> DNA
<213> Homo sapien

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```

<400> 260
ttttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaa at aagcaatggt      60
aaggtgtctt aacttgaaaa agattaggag tcaactggtt acaagttata attgaatgaa      120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaacia caggattaac      180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttataaac agactgattc      240
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca      300
c

```

```

<210> 261
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 261
aaatattcga gcaaatcctg taactaatgt gtctccataa aaggctttga actcagtga      60
tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggt      120
agcaccaact attccatata attcatcagc aggaaataaa ggctcttcag aagggttcaat      180
ggtgacatcc aatttcttct gataatttag attcctcaca accttcttag ttaagtgaag      240
ggcatgatga tcatccaaag ccagtggtc acttactcca gactttctgc aatgaagatc      300
a

```

```

<210> 262
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 262
gaggagagcc tgttacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc      60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaacc ctgagtcacc      120
cctagacttc ctaaaccaga tctctgggg ctggaacctg gcactctgca tttgtaatga      180
gggctttctg gtgcacacct aattttgtgc atctttgcc taaatcctgg attagtcccc      240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat      300
c

```

```

<210> 263
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

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<400> 263

tttagcttgt ggtaaatagac tcacaaaact gatttttaaaa tcaagttaat gtgaattttg 60
aaaattacta cttaatccta attcacaata acaatggcat taaggtttga cttgagttgg 120
ttcttagtat tatttatggg aaataggctc ttaccacttg caaataactg gccacatcat 180
taatgactga cttcccagta aggctctcta aggggtaagt angaggatcc acaggatttg 240
agatgctaag gccccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg 300
g 301

<210> 264

<211> 301

<212> DNA

<213> Homo sapien

<400> 264

aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaascc 60
aatgaatgac tctaaaaaca atatttacat ttaatggttt gtagacaata aaaaaacaag 120
gtggatagat ctagaattgt aacattttta gaaaaccata scatttgaca gatgagaaag 180
ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac 240
acccttcata taaattcact atcttggtt gaggcactcc ataaaatgta tcacgtgcat 300
a 301

<210> 265

<211> 301

<212> DNA

<213> Homo sapien

<400> 265

tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcatctttgt 60
cttcttgatga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta 120
catattcttg gaagtctcta atcaactttt gttccatttg tttcatttct tcaggagggg 180
tttccagttt gtcaacatgt tctctaaca cacttgccca tttctgtaaa gaatccaaag 240
cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg 300
c 301

<210> 266

<211> 301

<212> DNA

<213> Homo sapien

<400> 266

taccgtctgc ctttctccc atccaggcca tctgcgaatc tacatgggtc ctctatttcg 60
acaccagatc actcttttct ctaccacag gcttgctatg agcaagagac acaactctct 120
ctcttctgtg ttccagcttc ttttctgtt ctcccaccc cttaagttct attcctgggg 180
atagagacac caatacccat aacctctctc ctaagcctcc ttataaccca gggcgacag 240
cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgctg 300
a 301

<210> 267

<211> 301

<212> DNA

<213> Homo sapien

<400> 267

aaagagcaca ggccagctca gcctgccctg gccatctaga ctcagcctgg ctccatgggg 60

gtttctcagtg ctgagtccat ccaggaaaag ctcacctaga ctttctgagg ctgaatcttc 120
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatggctt ggagtaaagc 180
ctcattctga ttccctctct tcttttcttt caagttggct ttccctacat ccttctgttc 240
aattcgcttc agcttgcttg ctttagccct catttccaga agcttcttct ctttggcatc 300
t 301

<210> 268
<211> 301
<212> DNA
<213> Homo sapien

<400> 268
aatgtctcac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta 60
gatcttggga gagctgggtc ttctaaggag aaggaggaag gacagatgta actttggatc 120
tcgaagagga agtctaattg aagtaattag tcaacgggtc ttgtttagac tcttggata 180
tgctgggtgg ctgagtggc ccttttggag aaagcaagta ttattcttaa ggagtaacca 240
cttcccattg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact 300
a 301

<210> 269
<211> 301
<212> DNA
<213> Homo sapien

<400> 269
taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat 60
aaaattacct ttattcacac atctcaaac aattctgcaa attcttagtg aagtttaact 120
atagtcacag accttaaata ttcacattgt tttctatgtc tactgaaaat aagttcacta 180
cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta 240
tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc 300
t 301

<210> 270
<211> 301
<212> DNA
<213> Homo sapien

<400> 270
cattgaagag cttttgcaa acatcagaac acaagtgcct ataaaattaa ttaagcctta 60
cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120
gagcttgctg gtgcagtgca tattggataa cactattcat ggccgaattg atcaagtcaa 180
ccaactcctt gaactggatc atcagaagaa ggggtgtgca cgatatactg cactagataa 240
tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac 300
a 301

<210> 271
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (301)
<223> n = A,T,C or G

<400> 271

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aaaagggttct cataagatta acaattttaa taaatatttg atagaacatt ctttctcatt      60
tttatagctc atcttttaggg ttgatattca gtccatgctt cccttgctgt tcttgatcca     120
gaattgcaat cacttcatca gectgtattc gctccaattc tctataaagt ggggtccaagg     180
tgaaccacag agccacagca cacctctttc ccttggtgac tgccttcacc ccatganggt     240
tctctcctcc agatganaac tgatcatgcg ccacacattt ggggtttata gaagcagtca     300
c                                                                           301

```

<210> 272

<211> 301

<212> DNA

<213> Homo sapien

<400> 272

```

taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaagtgc      60
ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga     120
tccaataatt cctcatgat gagcaagaaa aattctttgc gcacccctcc tgcattccaca     180
gcatcttctc caacaaatat aaccttgagt ggcttcttgt aatctatgtt ctttggtttc     240
ctaaggactt ccattgcatc tctacaata ttttctctac gcaccactag aattaagcag     300
g                                                                           301

```

<210> 273

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 273

```

acatgtgtgt atgtgtatct ttgggaaaaa aanaagacat cttgtttayt atttttttgg      60
agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactyga      120
gaaccgtcta aaaataaaat ttaccatgtc dtatattcct tatagtatgc ttatttcacc     180
ttytttctgt ccagagagag tatcagtgc ananatttma ggggtgaamac atgmattgg      240
gggacttnty tttacngagm accctgcccg sgcgccctcg makngantt ccgcsananc     300
t                                                                           301

```

<210> 274

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 274

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cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttcttttgagg      60
aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa     120
tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttggt gaaaagtcca     180
tctaggtatg gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaagg      240
aattgtgctt cttttgataa gaagctttct tggatcatatc aggaaattcc aganaaagtc     300

```


c 301

<210> 275
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 275
tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg 60
gggtgaaatt ggccaacttt ctattaactt atgttggcaa ttttgccacc aacagtaagc 120
tggcccttct aataaaaagaa aattgaaagg tttctcacta aacggaatta agtagtggag 180
tcaagagact cccaggcctc agcgtacctg cccgggcggc cgctcgaagc cgaattctgc 240
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccttat 300
a 301

<210> 276
<211> 301
<212> DNA
<213> Homo sapien

<400> 276
tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat 60
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat 120
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc 180
caatacatTT aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt 240
aaaactatTC agtatgttTC ctttgcttca tgtctgagaa ggctctcctt caatggggat 300
g 301

<210> 277
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 277
tttgttgatg tcagtattttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60
atacagagga cttggaggaa gcagagcaac tgaattttaat ttaaaagaag gaaaacattg 120
gaatcatggc actcctgata ctttcccaaa tcaacactct caatgccccca ccctcgctct 180
caccatagtg gggagactaa agtggccacg gatttgcctt angtgtgcag tgcgttctga 240
gttcnctgtc gattacatct gaccagtctc ctttttccga agtccttcg ttcaatcttg 300
c 301

<210> 278
<211> 301
<212> DNA
<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 278
 taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60
 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120
 cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180
 aatgaacatc tcatgtgtgc tcacaatgtt ctggcactat tataagtgtc tcacagggtt 240
 tatgtgttct tcgtaacttt atggantagg tactcggcgc cgaacacgct aagccgaatt 300
 c 301

<210> 279
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 279
 aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60
 gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120
 ttagaccttt accttccagc caccacacag tgcttgatat ttcagagtca gtcattgggt 180
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300
 a 301

<210> 280
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 280
 ggtactggag ttttctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60
 tagaaagggt gtggaaccaa attgtggtca atggaaatag gagaatatgg ttctcactct 120
 tgagaaaaaa acctaaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180
 gtttgatata gtttaggggt ggggttagat taagatctaa attacatcag gacaaagaga 240
 cagactatta actccacagt taattaagga ggtatgttcc atgtttatatt gttaaagcag 300
 t 301

<210> 281
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 281
 aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatattc 60
 gccgagcaat ccaaatcctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120
 atgtggtagc aatggcttta tcgggttata cggatgagaa gaactccctt tggagagaaa 180
 tgtgtagcac actgcgatta cagctaaata acccgatatt gtgtgtcatg tttgcatttc 240

tgacaagtga aacaggatct tacgatggag ttttgtatga aaacaaagtt gcagtacctc 300
g 301

<210> 282

<211> 301

<212> DNA

<213> Homo sapien

<400> 282

cagggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60
tccagaaccc aaaaattaaag aaattcaaaa agacattttg tgggcacctg ctagcacaga 120
agcgcagaag caaagcccag gcagaacctat gctaacccta cagctcagcc tgcacagaag 180
cgcagaagca aagcccaggc agaacctatg taaccttaca gctcagcctg cacagaagcg 240
cagaagcaaa gccccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300
a 301

<210> 283

<211> 301

<212> DNA

<213> Homo sapien

<400> 283

atctgtatac ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaaag 60
cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120
gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180
acttcccagg ttttatgcaa aaattttgtt aaattctata atggatgatat gcattcttta 240
ggaaacatat acatttttta aaattctatt tatgtaagaa ctgacagacg aatttgcttt 300
g 301

<210> 284

<211> 301

<212> DNA

<213> Homo sapien

<400> 284

cagggtacaaa acgctattaa gtggcttaga atttgaacat ttgtggtctt tatttacttt 60
gcttcgtgtg tgggcaaagc aacatcttcc ctaaataat attaccaaga aaagcaagaa 120
gcagattagg tttttgacaa aacaaacagg ccaaaagggg gctgacctgg agcagagcat 180
ggtgagaggc aaggcatgag agggcaagtt tggtgtggac agatctgtgc ctactttatt 240
actggagtaa aagaaaacaa agttcattga tgctgaagga tatatacagt gttagaaatt 300
a 301

<210> 285

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 285

acatcaccat gatcggtacc cccacccatt atacgttgta tgtttacata aatactcttc 60
aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac 120

caggaaagca aatgctatctt acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180
attaaatatg tctgacttct tttaggtca cagactagg caaatgctat ttacgatctg 240
caaaagctgt ttgaagagtc aaagcccca tgtgaacacg atttctggac cctgtaacag 300
t 301

<210> 286

<211> 301

<212> DNA

<213> Homo sapien

<400> 286

taccactgca ttccagcctg ggtgacagag tgagactcgg tctccaaaaa aaactttgct 60
tgtatattat ttttgcttta cagtggatca ttctagtagg aaaggacagt aagatttttt 120
atcaaaatgt gtcattgccag taagagatgt tatattcttt tctcatttct tccccacca 180
aaaataagct accatatagc ttataagtct caaatttttg ctttttacta aaatgtgatt 240
gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt ttttcccttg 300
t 301

<210> 287

<211> 301

<212> DNA

<213> Homo sapien

<400> 287

tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60
cccagaagga acgtagagat cagatattac aacagctttg ttttgagggg tagaaatatg 120
aaatgatttg gttatgaacg cacagtttag gcagcagggc cagaatcctg accctctgcc 180
ccgtgggtat ctctcccca gcttggctgc ctcatgttat cacagtattc cattttgttt 240
gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc 300
t 301

<210> 288

<211> 301

<212> DNA

<213> Homo sapien

<400> 288

gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60
agtcaatagg aagacaaatt ccagttccag ctcatgtctg gtatctgcaa agctgcaaaa 120
gatcttttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac 180
aaaagcatct gcttttgtga tttaatttag ctcatctggc cactggaaga atccaaacag 240
tctgccttaa ttttgatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
a 301

<210> 289

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (301)

<223> n = A,T,C or G

<400> 289

ggtagactgt	ttccatgtta	tgtttctaca	cattgctacc	tcagtgtccc	tgaaactta	60
gcttttgatg	tctccaagta	gtccaccttc	atttaactct	ttgaaactgt	atcatctttg	120
ccaagtaaga	gtggtggcct	atttcagctg	ctttgacaaa	atgactggct	cctgacttaa	180
cgttctataa	atgaatgtgc	tgaagcaaag	tgcccatggg	ggcggcgaa	aagagaaaga	240
tgtgttttgt	tttggaactc	ctgtgggtcc	ttccaatgct	gtgggtttcc	aaccagnnga	300
a						301

<210> 290

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

 $\langle 222 \rangle \quad (1) \dots (301)$

<223> n = A,T,C or G

<400> 290

acactgagct	cttcttgata	aatatacaga	atgcttggca	tatacaagat	tctatactac	60
tgactgatct	gttcatttct	ctcacagctc	ttaccccca	aagcttttcc	accctaagtg	120
ttctgacctc	ctttttcta	cacagttagg	atagaggcag	anccacctac	aatgaacatg	180
gagttctatc	aagaggcaga	aacagcacag	aatcccagtt	ttaccattcg	ctagcagtg	240
tgccctgaac	aaaaacattt	ctccatgtct	cattttcttc	atgcctcaag	taacagtgag	300
a						301

<210> 291

<211> 301

<212> DNA

<213> Homo sapien

<400> 291

caggtagctaa	tttcttctat	cctagaaaca	tttcatttta	tgttgttgaa	acataacaac	60
tatatcagct	agattttttt	tctatgcttt	acctgctatg	gaaaaattga	cacattctgc	120
tttactcttt	tgtttatagg	tgaatcacia	aatgtatttt	tatgtattct	gtagttcaat	180
agccatggct	gtttacttca	tttaatttat	ttagcataaa	gacattatga	aaaggcctaa	240
acatgagctt	cacttcccca	ctaactaatt	agcatctgtt	atttcttaac	cgtaatgcct	300
a						301

<210> 292

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

 $\langle 222 \rangle \quad (1) \dots (301)$

<223> n = A, T, C or G

<400> 292

accttttagt	agtaatgtct	aataataaat	aagaatcaa	ttttataagg	tccatatagc	60
tgtattaaat	aatttttaag	tttaaaagat	aaaataccat	catttttaaat	gttggtattc	120
aaaaccaaag	natataaccg	aaaggaaaaa	cagatgagac	ataaaatgat	ttcgnagatg	180
ggaaatatag	tasttyatga	atgttnatta	aattccagtt	ataatagtgg	ctacacactc	240
tcactacaca	cacagacccc	acagtcctat	atgccacaaa	cacattttcca	taacttgaaa	300
a						301

<210> 293
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 293
 ggtaccaagt gctggtgccg gcctgttacc tgttctcact gaaaagtctg gctaattgctc 60
 ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcctagagc actgactgtt 120
 aacacaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt 180
 gtgagaattt tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg 240
 ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat 300
 g 301

<210> 294
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 294
 tgacccataa caatatacac tagctatctt ttttaactgtc catcattagc accaatgaag 60
 attcaataaa attaccttta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag 120
 ttttaactata gtcacaganc ttaaattatc acattgtttt ctatgtctac tgaaaataag 180
 ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240
 cccaattata cagtagcaca accaccttat gtagttttta catgatatgct ctgtagaggt 300
 t 301

<210> 295
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 295
 gtactctttc tctcccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta 60
 cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac 120
 ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccattctctga 180
 actggtagaa aaacrtctga agagctagtc tatcagcadc tgacaggtga attggatggt 240
 tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttggtt 300
 tctct 305

<210> 296
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 296
 aggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct 60
 cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg 120
 attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac 180
 tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt 240

tgctattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg 300
c 301

<210> 297

<211> 300

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(300)

<223> n = A,T,C or G

<400> 297

actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta 60
aaggttttga aaaccttgaa ggagaatcat tttgacaaga agtacttaag agtctagaga 120
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt 180
tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggtc 240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc acactggcgg 300

<210> 298

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 298

tatgggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc ccctcccgcg 60
ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgccggctg 120
tgaagctctc agatcaatca cgggaagggc ctggcggtgg tggccacctg gaaccaccct 180
gtcctgtctg tttacatttc actaycaggt tttctctggg cattacnatt tgttccccta 240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcagggtggct ctcagcgagg 300
t 301

<210> 299

<211> 301

<212> DNA

<213> Homo sapien

<400> 299

gttttgagac ggagtttcac tcttggtgcc cagactggac tgcaatggca gggctctctgc 60
tcactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct cccaggtagc 120
tgggattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg 180
gagtttcgcc atgttgacca gctggcttca aactcctgac ctcaagcgac ctgcctgcct 240
cggcctccca aagtgttgga attataggca tgagtcaaca cgcccagcct aaagatattt 300
t 301

<210> 300

<211> 301

<212> DNA

<213> Homo sapien

<400> 300

attcagtttt atttgctgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga	60
tatgtccac acccactggg aaaggctccc acctggctac ttcctctatc agctgggtca	120
gctgcattcc acaaggttct cagcctaata agtttacta cctgccagtc tcaaaactta	180
gtaaagcaag accatgacat tccccacgg aaatcagagt ttgccccacc gtcttggtac	240
tataaagcct gcctctaaca gtccttgctt cttcacacca atccccgagc catcccccat	300
g	301

<210> 301

<211> 301

<212> DNA

<213> Homo sapien

<400> 301

ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc	60
agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagtgtgt	120
gggaactcac aaagaccctc agagctgaga caccacaac agtgggagct cacaagacc	180
ctcagagctg agacaccac aacagtggga gtcacaaag accctcagag ctgagacacc	240
cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt	300
t	301

<210> 302

<211> 301

<212> DNA

<213> Homo sapien

<400> 302

aggtacacat ttagcttggt gtaaatgact cacaaaactg attttaaaat caagttaatg	60
tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac	120
ttgagttggt tcttagtatt atttatggta aataggtctt taccacttgc aaataactgg	180
ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca	240
caggatttga gatgctaagg cccagagat cgtttgatcc aacctctta ttttcagagg	300
g	301

<210> 303

<211> 301

<212> DNA

<213> Homo sapien

<400> 303

aggtaccaac tgtggaaata ggtagaggat cattttttct tccatatca actaagttgt	60
atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac	120
tggctaattg aactaccgct tgcattgtaa aaatgggtgt ttgtgaaatg atcataggcc	180
agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc	240
catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac	300
c	301

<210> 304

<211> 301

<212> DNA

<213> Homo sapien

<400> 304

acatggatgt tattttgcag actgtcaacc tgaatttgta tttgcttgac attgccta	60
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tattagtttc agtttcagct taccacattt ttgtctgcaa catgcaraas agacagtgcc      120
cttttttagtg tatcatatca ggaatcatct cacattgggt tgtgccatta ctgggtgcagt      180
gacttttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga      240
ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct      300
c                                                                              301

```

<210> 305

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 305

```

gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag      60
caggggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggag      120
taaaggagga gaaacagata caaaatctcc aactcagtat taaggatttc tcatgcctag      180
aatattggta gaaacaagaa tacattcata tggcaaataa ctaaccatgg tggacaacaaa      240
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag      300
a                                                                              301

```

<210> 306

<211> 8

<212> PRT

<213> Homo sapien

<400> 306

```

Val Leu Gly Trp Val Ala Glu Leu
1           5

```

<210> 307

<211> 637

<212> DNA

<213> Homo sapien

<400> 307

```

acaggggatg aagggaaagg gagaggatga ggaagccccc ctggggattt ggtttgggtcc      60
ttgtgatcag gtggtctatg gggcttatcc ctacaaagaa gaatccagaa atagggggcac      120
attgaggaat gatacttgag cccaaagagc attcaatcat tgttttattt gccttmtttt      180
cacaccattg gtgagggagg gattaccacc ctggggttat gaagatgggt gaacacccca      240
cacatagcac cggagatatg agatcaacag tttcttagcc atagagattc acagcccaga      300
gcaggaggac gcttgcacac catgcaggat gacatggggg atgcgctcgg gattggtgtg      360
aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacggtgggg caaactctga      420
ttccgtggg ggaatgtcat ggtcttgctt tactaagttt tgagactggc aggtagtga      480
actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatagag gaagtagcca      540
ggtgggagcc tttccagtg ggtgtgggac atatctggca agattttgtg gcactcctgg      600
ttacagatac tggggcagca aataaaactg aatcttg                                     637

```

<210> 308

<211> 647

<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(647)
<223> n = A,T,C or G

<400> 308

acgattttca	ttatcatgta	aatcgggtca	ctcaaggggc	caaccacagc	tgggagccac	60
tgctcagggg	aaggttcata	tgggactttc	tactgcccaa	ggttctatac	aggatataaa	120
ggngcctcac	agtatagatc	tggtagcaaa	gaagaagaaa	caaacactga	tctctttctg	180
ccaccctctt	gacccttttg	aactcctctg	acccttttaga	acaagcctac	ctaatatctg	240
ctagagaaaa	gaccaacaac	ggcctcaaag	gatctcttac	catgaaggtc	tcagctaatt	300
cttggctaag	atgtgggttc	cacattaggt	tctgaatatg	gggggaaggg	tcaatttgct	360
cattttgtgt	gtggataaag	tcaggatgcc	cagggggccag	agcagggggc	tgcttgcttt	420
gggaacaatg	gctgagcata	taaccatagg	ttatggggaa	caaaacaaca	tcaaagtcac	480
tgtatcaatt	gccatgaaga	cttgagggac	ctgaatctac	cgattcatct	taaggcagca	540
ggaccagttt	gagtggcaac	aatgcagcag	cagaatcaat	ggaaacaaca	gaatgattgc	600
aatgtccttt	tttttctcct	gcttctgact	tgataaaaag	ggaccgt		647

<210> 309
<211> 460
<212> DNA
<213> Homo sapien

<400> 309

actttatagt	ttaggctgga	cattggaaaa	aaaaaaaaagc	cagaacaaca	tgtgatagat	60
aatatgattg	gctgcacact	tccagactga	tgaatgatga	acgtgatgga	ctattgtatg	120
gagcacatct	tcagcaagag	ggggaaatac	tcattcatttt	tggccagcag	ttgtttgatc	180
accaaacatc	atgccagaat	actcagcaaa	ccttcttagc	tcttgagaag	tcaaagtccg	240
ggggaattta	ttcctggcaa	ttttaattgg	actccttatg	tgagagcagc	ggctaccag	300
ctgggggtgt	ggagcgaacc	cgctactagt	ggacatgcag	tggcagagct	cctggtaacc	360
acctagagga	atacacaggc	acatgtgtga	tgccaagcgt	gacacctgta	gcactcaaat	420
ttgtcttggt	tttgtctttc	ggtgtgtaag	attcttaagt			460

<210> 310
<211> 539
<212> DNA
<213> Homo sapien

<400> 310

acgggactta	tcaaataaag	ataggaaaag	aagaaaactc	aaatattata	ggcagaaatg	60
ctaaagggtt	taaaatatgt	caggattgga	agaaggcatg	gataaagaac	aaagttcagt	120
taggaaagag	aaacacagaa	ggaagagaca	caataaaagt	cattatgtat	tctgtgagaa	180
gtcagacagt	aagattttgt	ggaaatgggt	tggtttgttg	tatggtatgt	atttttagcaa	240
taatctttat	ggcagagaaa	gctaaaatcc	tttagcttgc	gtgaatgac	acttgctgaa	300
ttcctcaagg	taggcatgat	gaaggaggg	ttagaggaga	cacagacaca	atgaactgac	360
ctagatagaa	agccttagta	tactcagcta	ggaatagtga	ttctgagggc	acactgtgac	420
atgattatgt	cattacatgt	atggtagtga	tggggatgat	aggaaggaag	aacttatggc	480
atattttcac	ccccacaaaa	gtcagttaaa	tattggggaca	ctaaccatcc	aggtcaaga	539

<210> 311
<211> 526
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (526)
<223> n = A,T,C or G

<400> 311
caaatTTgag ccaatgacat agaattttac aaatcaagaa gcttattctg gggccatttc 60
ttttgacgtt ttctctaaac tactaaagag gcattaatga tccataaatt atattatcta 120
catttacagc atttaaaatg tgttcagcat gaaatattag ctacagggga agctaaataa 180
attaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg 240
tttttcacaa gtgaagcatt cttataaagt gtcataacct ttttggggaa actatgggaa 300
aaaatgggga aactctgaag ggttttaagt atcttacctg aagctacaga ctccataacc 360
tctctttaca gggagctcct gcagccctta cagaaatgag tggctgagat tcttgattgc 420
acagcaagag cttctcatct aaaccctttc cctttttagt atctgtgtat caagtataaa 480
agttctataa actgtagtnt acttatttta atccccaag cacagt 526

<210> 312
<211> 500
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (500)
<223> n = A,T,C or G

<400> 312
cctctctctc cccacccct gactctagag aactgggttt tctccagta ctccagcaat 60
tcatttctga aagcagttga gccactttat tccaaagtac actgcagatg ttcaaactct 120
ccatttctct ttcccttcca cctgccagtt ttgctgactc tcaacttgct atgagtgtaa 180
gcattaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg 240
gcttcttagg aaaatatttt tcttccaaaa tcagtaggaa atctaaactt atccccctct 300
tgcagatgtc tagcagcttc agacatttgg ttaagaacct atgggaaaaa aaaaaatcct 360
tgctaattgt gtttcctttg taaaccanga ttcttatttg nctggatatag aatatcagct 420
ctgaacgtgt ggtaaagatt tttgtgtttg aatataggag aaatcagttt gctgaaaagt 480
tagtcttaat tatctattgg 500

<210> 313
<211> 718
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (718)
<223> n = A,T,C or G

<400> 313
ggagatttgt gtggtttgca gccgaggag accaggaaga tctgcatggt gggaaggacc 60
tgatgataca gaggtgagaa ataagaaagg ctgctgactt taccatctga ggccacacat 120
ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata taatgtctaa 180
gtagtacat gtttttgac atttccagcc cttttaaata tccacacaca caggaagcac 240
aaaaggagc acagagatcc ctgggagaaa tgcccggccg ccatcttggg tcatcgatga 300
gcctcgccct gtgcctgntc ccgcttgtga gggaaggaca ttagaaaatg aattgatgtg 360
ttccttaaag gatggcagga aaacagatcc tgttgtggat atttatttga acgggattac 420

agatttgaaa tgaagtcaca aagtgagcat taccaatgag aggaaaacag acgagaaaat	480
cttgatgggt cacaagacat gcaacaaaca aaatggaata ctgtgatgac acgagcagcc	540
aactggggag gagataccac ggggcagagg tcaggattct ggccctgctg cctaactgtg	600
cgttatacca atcatttcta tttctaccct caaacaagct gtngaatatc tgacttacgg	660
ttctnttggc ccacatttcc atnatccacc cntcntttt aannttantic caaantgt	718

<210> 314

<211> 358

<212> DNA

<213> Homo sapien

<400> 314

gtttatttac attacagaaa aaacatcaag acaatgtata ctatttcaaa tatatccata	60
cataatcaaa tatagctgta gtacatgttt tcattgggtg agattaccac aaatgcaagg	120
caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg tgtagtccaa	180
gctctcggta gtccagccac tgtgaaacat gctcccttta gattaacctc gtggacgctc	240
ttgttgatt gctgaactgt agtgccctgt attttgcttc tgtctgtgaa ttctgttgct	300
tctggggcat ttccttgtga tgcagaggac caccacacag atgacagcaa tctgaatt	358

<210> 315

<211> 341

<212> DNA

<213> Homo sapien

<400> 315

taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc	60
ataggtgatg atgaggacat ggaatgggcc cccaaggatg gtctgtccaa agaagcgagt	120
gacccccatt ctgaagatgt ctggaacctc taccagcagg atgatgatag cccaatgac	180
agtcaccagc tccccgacca gccggatata gtccttaggg gtcattgtag ctctctgaag	240
tagcttctgc tgtaagaggg tgttgctccc ggggctcgtg cggttattgg tcctgggctt	300
gagggggcgg tagatgcagc acatgggtgaa gcagatgatg t	341

<210> 316

<211> 151

<212> DNA

<213> Homo sapien

<400> 316

agactgggca agactcttac gcccacact gcaatttggt cttgttgccg tatecattta	60
tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact	120
cattcagggg gctctgggtg caatattagt t	151

<210> 317

<211> 151

<212> DNA

<213> Homo sapien

<400> 317

agaactagtg gatacctaag aaatacctga aacatatatt ggcatttata aatggctcaa	60
atcttcattt atctctggcc ttaaccctgg ctcctgaggg tgcggccagc agatcccagg	120
ccagggtctt gttcttgcca cacctgcttg a	151

<210> 318

<211> 151

<212> DNA

<213> Homo sapien

<400> 318

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actggtggga ggcgctgttt agttggctgt tttcagaggg gtctttcgga gggacctcct    60
gctgcaggct ggagtgtctt tttcctggc gggagaccgc acattccact gctgaggctg    120
tgggggcggg ttatcaggca gtgataaaca t                                  151
```

<210> 319

<211> 151

<212> DNA

<213> Homo sapien

<400> 319

```
aactagtgga tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta    60
catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg    120
taagattggg tttatgtgat tttagtgggt a                                  151
```

<210> 320

<211> 150

<212> DNA

<213> Homo sapien

<400> 320

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aactagtgga tccactagtc cagtgtgggt gaattccatt gtgttggggg tctagatcgc    60
gagcggctgc cttttttttt tttttttttg ggggggaatt tttttttttt aatagttatt    120
gagtgttcta cagcttacag taaataccat                                  150
```

<210> 321

<211> 151

<212> DNA

<213> Homo sapien

<400> 321

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agcaactttg tttttcatcc aggttatatt aggcttagga tttcctctca cactgcagtt    60
taggggtggc ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg    120
tgctctgag aaatcaaagt cttcatacac t                                  151
```

<210> 322

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 322

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atccagcate ttctcctgtt tcttgcttc cttttcttc ttcttasatt ctgcttgagg    60
tttgggcttg gtcagtttgc cacagggtt ggagatggtg acagtcttct ggcattcggc    120
attgtgcagg gctcgttca nacttccagt t                                  151
```

<210> 323

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 323

tgaggacttg tktctctttt ctttattttt aatcctctta ckttgtaa atattgccta	60
nagactcant tactaccag tttgtgggtt twtgggagaa atgtaactgg acagtttagct	120
gttcaatyaa aaagacactt ancccatgtg g	151

<210> 324

<211> 461

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(461)

<223> n = A,T,C or G

<400> 324

acctgtgtgg aatttcagct ttcctcatgc aaaaggattt tgtatccccg gcctacttga	60
agaagtgggc agctaaagga atccagggtt tgggttggac tgtaataacc tttgatgaaa	120
agagttacta cgaatcccat cttgggtcca gctatatcac tgacagcatg gtagaagact	180
gcgaacctca cttctagact ttcacgggtg gacgaaacgg gtccagaaac tgccaggggc	240
ctcatacagg gatatacaaaa taccctttgt gctaccagg cctgggggaa tcaggtgact	300
cacacaaatg caatagttgg tcaactgcatt tttacctgaa ccaaagctaa acccgggtgt	360
gccaccatgc accatggcat gccagagttc aacactgttg ctcttgaaaa ttgggtctga	420
aaaaacgcac aagagcccct gccctgccct agctgangca c	461

<210> 325

<211> 400

<212> DNA

<213> Homo sapien

<400> 325

acactgtttc catgttatgt ttctacacat tgctacctca gtgctcctgg aaacttagct	60
tttgatgtct ccaagtagtc caccttcatt taactctttg aaactgtatc atctttgcc	120
agtaagagtg gtggcctatt tcagctgctt tgacaaaatg actggctcct gacttaacgt	180
tctataaatg aatgtgctga agcaaagtgc ccatgggtggc ggcgaagaag agaaagatgt	240
gttttgttt ggactctctg tggctccttc caatgctgtg ggtttccaac caggggaagg	300
gtcccttttg cattgccaag tgccataacc atgagcacta cgctaccatg gttctgcctc	360
ctggccaagc aggtgggtt gcaagaatga aatgaatgat	400

<210> 326

<211> 1215

<212> DNA

<213> Homo sapien

<400> 326

ggaggactgc agcccgact cgcagccctg gcaggcggca ctgggtcatgg aaaacgaatt	60
gttctgctcg ggcgtcctgg tgcattccgca gtgggtgctg tcagccgcac actgtttcca	120
gaactcctac accatcgggc tgggcctgca cagtcttgag gccgaccaag agccagggag	180

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ccagatggtg gaggccagcc tctccgtacg gcacccagag tacaacagac ccttgctcgc      240
taacgacctc atgctcatca agttggacga atccgtgtcc gagtctgaca ccatccggag      300
catcagcatt gcttcgcagt gccctaccgc ggggaactct tgcctcgttt ctggctgggg      360
tctgctggcg aacggcagaa tgcctaccgt gctgcagtgc gtgaacgtgt cgggtggtgtc      420
tgaggaggtc tgcagtaagc tctatgaccc gctgtaccac cccagcatgt tctgcgccgg      480
cggaggggcaa gaccagaagg actcctgcaa cggtgactct ggggggcccc tgatctgcaa      540
cgggtacttg cagggccttg tgtctttcgg aaaagccccg tgtggccaag ttggcgtgcc      600
aggtgtctac accaacctct gcaaattcac tgagtggata gagaaaaccg tccaggccag      660
ttaactctgg ggactgggaa cccatgaaat tgaccccaa atacatcctg cggaaggaaat      720
tcaggaatat ctgttcccag cccctcctcc ctcaggccca ggagtccagg ccccagccc      780
ctcctccttc aaaccaaggg tacagatccc cagccctcc tccctcagag ccaggagtcc      840
agaccccca gccctcctc cctcagaccc aggagtccag cccctcctcc ctcagacca      900
ggagtccaga cccccagcc cctcctcctc cagaccagg ggtccaggcc cccaaccct      960
cctcctcag actcagaggt ccaagcccc aaccctcct tcccagacc cagaggtcca     1020
ggtcccagcc cctcctcctc cagaccagc ggtccaatgc cacctagact ctcctgtac     1080
acagtgcccc cttgtggcac gttgaccaa cttaccagt tggttttca tttttgtcc     1140
ctttcccta gatccagaaa taaagtctaa gagaagcgca aaaaaaaaaa aaaaaaaaaa     1200
aaaaaaaaa aaaaaa                                         1215

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<210> 327

<211> 220

<212> PRT

<213> Homo sapien

<400> 327

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Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
 1          5          10          15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
          20          25          30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
 35          40          45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
 50          55          60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
 65          70          75          80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
          85          90          95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
 100          105          110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
 115          120          125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
 130          135          140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
 145          150          155          160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
          165          170          175
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 <213> Homo sapien

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 <212> PRT
 <213> Homo sapien

<400> 329
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 <212> DNA
 <213> Homo sapien

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 <213> Homo sapien

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<211> 3030

<212> DNA

<213> Homo sapien

<400> 333

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<211> 2417

<212> DNA

<213> Homo sapien

<400> 334

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<211> 2984

<212> DNA

<213> Homo sapien

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<210> 336

<211> 147

<212> PRT

<213> Homo sapien

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 <213> Homo sapien

<400> 337
 Ala Leu Thr Gly Phe Thr Phe Ser Ala
 1 5

<210> 338
 <211> 9
 <212> PRT
 <213> Homo sapien

<400> 338
 Leu Leu Ala Asn Asp Leu Met Leu Ile
 1 5

<210> 339
 <211> 318
 <212> PRT
 <213> Homo sapien

<400> 339
 Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Pro Phe Leu
 1 5 10 15
 Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
 20 25 30
 Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
 50 55 60
 Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
 65 70 75 80
 Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
 85 90 95
 Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
 100 105 110
 Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
 115 120 125
 Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
 130 135 140
 His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu

145 150 155 160
 Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
 165 170 175
 Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
 180 185 190
 Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala
 195 200 205
 Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly
 210 215 220
 Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val
 225 230 235 240
 Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe
 245 250 255
 Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu
 260 265 270
 Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His
 275 280 285
 Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg
 290 295 300
 Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
 305 310 315

<210> 340

<211> 483

<212> DNA

<213> Homo sapien

<400> 340

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 ctctgctgc aggcctggagt gtctttattc ctggcgggag accgcacatt cactgctga 180
 ggttggtggg gcggtttatc aggcagtgat aaacataaga tgtcatttcc ttgactccgg 240
 ccttcaattt tctctttggc tgacgacgga gtccgtggtg tcccgatgta actgaccct 300
 gctccaaacg tgacatcact gatgctcttc tgggggtgct tgatggcccg cttgggtcacg 360
 tgctcaatct cgccattcga ctcttgctcc aaactgtatg aagacacctg actgcacgtt 420
 tttctgggct ttccagaatt taaagtgaag ggcagcactc ctaagctccg actccgatgc 480
 ctg 483

<210> 341

<211> 344

<212> DNA

<213> Homo sapien

<400> 341

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 ttttttact aaccattcta tttttataga aatagctgag agtttctaaa ccaactctct 120
 gctgccttac aagtattaaa tttttactt ctttccataa agagtagctc aaaatagca 180
 attaatataa taatttctga tgatggtttt atctgcagta atatgtatat catctattag 240
 aatttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc 300
 ctgattctta acattgtctt taatgaccac aagacaacca acag 344

<210> 342

<211> 592

<212> DNA

<213> Homo sapien

<400> 342

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caatgtggaa	acttcttata	cttggttcca	ttatgaagtt	ggacaattgc	tgctatcaca	120
cctggcaggt	aaaccaatgc	caagagagtg	atggaaacca	ttggcaagac	tttgttgatg	180
accaggattg	gaattttata	aaaatattgt	tgatgggaag	ttgctaaagg	gtgaattact	240
tccctcagaa	gagtgtaaag	aaaagtcaga	gatgctataa	tagcagctat	tttaattggc	300
aagtgccact	gtggaaagag	ttcctgtgtg	tgctgaagtt	ctgaagggca	gtcaaattca	360
tcagcatggg	ctgtttggtg	caaatgcaaa	agcacaggtc	tttttagcat	gctggtctct	420
cccgtgtcct	tatgcaaata	atcgtcttct	tctaaatttc	tcctaggctt	cattttccaa	480
agttcttctt	ggtttgtgat	gtcttttctg	ctttccatta	attctataaa	atagtatggc	540
ttcagccacc	cactcttcgc	cttagcttga	ccgtgagtc	cggctgccgc	tg	592

<210> 343

<211> 382

<212> DNA

<213> Homo sapien

<400> 343

ttcttgacct	cctcctcctt	caagctcaaa	caccacctcc	cttatccagg	accggcactt	60
cttaatgttt	gtggctttct	ctccagcctc	tcttaggagg	ggtaatggtg	gagttggcat	120
cttgtaactc	tcctttctcc	tttcttcccc	tttctctgcc	cgcctttccc	atcctgctgt	180
agacttcttg	attgtcagtc	tgtgtcacat	ccagtgattg	ttttggtttc	tgttcccttt	240
ctgactgccc	aaggggctca	gaaccccagc	aatcccttcc	tttccattacc	ttcttttttg	300
ggggtagttg	gaagggactg	aaattgtggg	gggaaggtag	gaggcacatc	aataaagagg	360
aaaccaccaa	gctgaaaaaa	aa				382

<210> 344

<211> 536

<212> DNA

<213> Homo sapien

<400> 344

ctgggcctga	agctgtaggg	taaatcagag	gcaggcttct	gagtgatgag	agtcctgaga	60
caataggcca	cataaacttg	gctggatgga	acctcacaat	aagggtgtca	cctcttgttt	120
gtttaggggg	atgccaagga	taaggccagc	tcagttatat	gaagagaagc	agaacaaaca	180
agtctttcag	agaaatggat	gcaatcagag	tgggatcccg	gtcacatcaa	ggtcacactc	240
caccttcattg	tgctgaatg	gttgccaggt	cagaaaaatc	cacctcttac	gagtgcggct	300
tcgaccctat	atcccccgcc	cgcgtccctt	tctccataaa	attcttctta	gtagctatta	360
ccttcttatt	atttgatcta	gaaattgccc	tccttttacc	cctaccatga	gcctacaaa	420
caactaacct	gccactaata	gttatgtcat	ccctcttatt	aatcatcatc	ctagccctaa	480
gtctggccta	tgagtgacta	caaaaaggat	tagactgagc	cgaataacaa	aaaaaa	536

<210> 345

<211> 251

<212> DNA

<213> Homo sapien

<400> 345

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gcgtgggcca	ggaaatcaca	tcctacactg	cccaggagcc	agacacattt	atggaacaga	180
aaataacata	tcggatttgg	agagacactg	ccaactggct	ggagattaat	ccggacactg	240
gtgccatttc	c					251

<210> 346
<211> 282
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(282)
<223> n = A,T,C or G

<400> 346
cgcgctctctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt 60
ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcaagtaca aattctggga 120
aggagacta tacctggctc ttgccctaag tgagagggtc tccctcccgc accaaaaaat 180
agaaaggctt tctatttcac tggcccaggt aggggggaagg agagtaactt tgagtctgtg 240
ggtctcatth cccaagggtgc cttcaatgct catnaaaacc aa 282

<210> 347
<211> 201
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(201)
<223> n = A,T,C or G

<400> 347
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taaataatac ttttaaaana ntactancag cttttaccta ngctcctaaa tgcttgtaaa 120
tctgagactg actggaccca ccagaccca gggcaaagat acatgttacc atatcatctt 180
tataaagaat tttttttgt c 201

<210> 348
<211> 251
<212> DNA
<213> Homo sapien

<400> 348
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agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgcccctg ggcaggcaga 120
aggagacact ccagcatgg aggagggtt atcttttcat cctaggtcag gtctacaatg 180
ggggaagggt ttattataga actccaaca gccacactca ctctgccac ccacccgatg 240
gcctgcctc c 251

<210> 349
<211> 251
<212> DNA
<213> Homo sapien

<400> 349
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aacccttgag gatgccagag ctatgggtcc agaacatggt gtggtattat caacagagtt 120
cagaagggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt 180
agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca 240

actcctgggtt t

251

<210> 350

<211> 908

<212> DNA

<213> Homo sapien

<400> 350

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cggctggaat	tgctctgggt	atgatgacag	agaaaatgat	ctcttctctt	gtgacaccaa	180
cacctgtaaa	tttgatgggg	aatgtttaag	aattggagac	actgtgactt	gcgtctgtca	240
gttcaagtgc	aacaatgact	atgtgcctgt	gtgtggctcc	aatggggaga	gctaccagaa	300
tgagtgttac	ctgcgacagg	ctgcatgcaa	acagcagagt	gagatacttg	tggtgtcaga	360
aggatcatgt	gccacagtcc	atgaaggctc	tggagaaaact	agcaaaaagg	agacatccac	420
ctgtgatatt	tgccagtttg	gtgcagaatg	tgacgaagat	gccgaggatg	tctggtgtgt	480
gtgtaatat	gactgttctc	aaaccaactt	caatcccctc	tgcgcttctg	atgggaaatc	540
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catgtctttg	ggctgatgtc	aagataacac	aactacaact	actaagtctg	aagatgggca	660
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ccacatacct	tgtccggaac	attacaatgg	cttctgcatg	catgggaagt	gtgagcattc	780
tatcaatatg	caggagccat	cttgcaggtg	tgatgctggt	tatactggac	aacactgtga	840
aaaaaaggac	tacagtgttc	tatacgttgt	tcccggctct	gtacgatttc	agtatgtctt	900
aatcgacg						908

<210> 351

<211> 472

<212> DNA

<213> Homo sapien

<400> 351

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gtcaaacc	aatgccattg	ttattgtgaa	ttaggattaa	gtagtaattt	tcaaaattca	120
cattaact	attttaaaat	cagwtttgyg	agtcattttac	cacaagctaa	atgtgtacac	180
tatgataaaa	acaaccattg	tattcctgtt	tttctaaaca	gtcctaattt	ctaactgt	240
atatatcctt	cgacatcaat	gaactttgtt	ttcttttact	ccagtaataa	agtaggcaca	300
gatctgtcca	caacaaactt	gccctctcat	gccttgcttc	tcaccatgct	ctgctccagg	360
tcagccccct	tttggcctgt	ttgttttgtc	aaaaacctaa	tctgcttctt	gcttttcttg	420
gtaatatata	tttagggaag	atgttgcttt	gcccacacac	gaagcaaagt	aa	472

<210> 352

<211> 251

<212> DNA

<213> Homo sapien

<400> 352

ctcaaagcta	atctctcggg	aatcaaacca	gaaaagggca	aggatcttag	gcatggtgga	60
tgtggataag	gccaggtcaa	tggctgcaag	catgcagaga	aagaggtaca	tcggagcgtg	120
caggctgcgt	tcctgcctta	cgatgaagac	cacgatgcag	tttccaaaca	ttgccactac	180
atacatggaa	aggaggggga	agccaaccca	gaaatgggct	ttctctaate	ctgggatacc	240
aataagcaca	a					251

<210> 353

<211> 436

<212> DNA

<213> Homo sapien

<400> 353

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gtatccaaaa gcaaaacagc agatatacaa aattaaagag acagaagata gacattaaca	180
gataaggcaa cttatacatt gacaatccaa atccaataca tttaaacatt tgggaaatga	240
gggggacaaa tggaagccar atcaaatttg tgtaaaacta ttcagtatgt tccccctgct	300
tcatgtctga raaggctctc ctttcaatgg ggatgacaaa ctccaaatgc cacacaaatg	360
ttaacagaat actagattca cactggaacg ggggtaaaga agaaattatt ttctataaaa	420
gggctcctaa tgtagt	436

<210> 354

<211> 854

<212> DNA

<213> Homo sapien

<400> 354

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caagtctgaa accaaatcta ggaaacatag gaaacgagcc aggcacaggg ctgggtgggcc	120
atcagggacc accctttggg ttgatatttt gcttaatctg catcttttga gtaagatcat	180
ctggcagtag aagctgttct ccaggtagat ttctctagct catgtacaaa aacatctctga	240
aggactttgt caggtgcctt gctaaaagcc agatgcgttc ggcacttctt tgggtctgagg	300
ttaattgcac acctacaggc actgggctca tgctttcaag tattttgtcc tcacttttagg	360
gtgagtgaat gatcccatat ataggagcac ttgggagaga tcatataaaa gctgactctt	420
gagtacatgc agtaatgggg tagatgtgtg ttgtgtgtct tcatctctgc aaggggtgctt	480
gttagggagt gtttccagga ggaacaagtc tgaaaccaat catgaaataa atggtaggtg	540
tgaactggaa aactaattca aaagagagat cgtgatatac gtgtgggtga tacaccttgg	600
caatatggaa ggctctaatt tgcccatatt tgaaataata attcagcttt ttgtaataca	660
aaataacaaa ggatttgagaa tcatgggtgtc taatgtataa aagaccagg aaacataaat	720
atatcaactg cataaatgta aaatgcatgt gacccaagaa ggccccaaag tggcagacaa	780
cattgtacct attttccctt ccaaaatgtg agcggcgggc ctgctgcttt caaggctgtc	840
acacgggatg tcag	854

<210> 355

<211> 676

<212> DNA

<213> Homo sapien

<400> 355

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cagggtcaaag ctgatctttc tggaatgtca ccaaccaagg gcctatatat atcaaaaagcc	120
atccacaagt catacctgga tgtcagcgaa gagggcacgg aggcagcagc agccactggg	180
gacagcatcg ctgtaaaaag cctaccaatg agagctcagt tcaaggcgaa ccaccccttc	240
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gtgactttcc cacggccaaa aagctgttca caccctacgc acctctgtgc ctgagtttgc	420
tcatctgcaa aatagggtcta ggatttcttc caaccatttc atgagttgtg aagctaaggc	480
tttgttaatc atggaaaaag gtagacttat gcagaaagcc tttctggctt tcttatctgt	540
ggtgtctcat ttgagtgtctg tccagtgaca tgatcaagtc aatgagtaaa attttaaggg	600
attagatttt cttgacttgt atgtatctgt gagatcttga ataagtgacc tgacatctct	660
gcttaaagaa aaccag	676

<210> 356

<211> 574

<212> DNA

<213> Homo sapien

<400> 356

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caagcttccc	attttagat	ctcagtgcct	atgagtatct	gacacctgtt	cctctcttca	180
gtctcttagg	gaggcttaaa	tctgtctcag	gtgtgctaag	agtgccagcc	caaggkggtc	240
aaaagtcac	aaaactgcag	tctttgctgg	gatagtaagc	caagcagtgc	ctggacagca	300
gagttctttt	cttgggcaac	agataaccag	acaggactct	aatcgtgctc	ttattcaaca	360
ttcttctgtc	tctgcctaga	ctggaataaa	aagccaatct	ctctcgtggc	acaggggaagg	420
agatacaagc	tcgtttacat	gtgatagatc	taacaaaggc	atctaccgaa	gtctggtctg	480
gatagacggc	acagggagct	cttaggtcag	cgctgctggg	tggaggacat	tcctgagtc	540
agctttgcag	cctttgtgca	acagtacttt	ccca			574

<210> 357

<211> 393

<212> DNA

<213> Homo sapien

<400> 357

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taatatggkg	kcttggtcac	tatacttaaa	aatgcaccac	tcataaatat	ttaattcagc	120
aagccacaac	caaracttga	ttttatcaac	aaaaaccctt	aatataaac	ggsaaaaaag	180
atagataata	ttattccagt	ttttttaaaa	cttaaaarat	attccattgc	cgaattaara	240
araarataag	tggttatatg	aaagaagggc	attcaagcac	actaaaraaa	cctgaggkaa	300
gcataatctg	tacaaaatta	aactgtcctt	tttggcattt	taacaaattt	gcaacgktct	360
tttttttctt	tttctgtttt	tttttttttt	tac			393

<210> 358

<211> 630

<212> DNA

<213> Homo sapien

<400> 358

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gcatagagta	gggaagctaa	tccagcacag	ggaggtcaca	gagacatccc	taaggaagtg	180
gagtttaaac	tgagagaagc	aagtgcctaa	actgaaggat	gtgttgaaga	agaagggaga	240
gtagaacaat	ttgggcagag	ggaaccttat	agaccctaag	gtgggaagg	tcaaagaact	300
gaaagagagc	tagaacagct	ggagccgttc	tccggtgtaa	agaggagtca	aagagataag	360
attaaagatg	tgaagattaa	gatcttggtg	gcattcaggg	attggcactt	ctacaagaaa	420
tcaactgaagg	gagtaatgtg	acattacttt	tcacttcagg	atggccattc	taactccagg	480
gggtagactg	gactaggtaa	gactggaggc	aggtagacct	cttctaaggc	ctgcgatagt	540
gaaagacaaa	aataagtggg	gaaattcagg	ggatagtgaa	aatcagtagg	acttaatgag	600
caagccagag	gttctctcac	aacaaccagt				630

<210> 359

<211> 620

<212> DNA

<213> Homo sapien

<400> 359

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taattaaaaa	atgctactaa	tatagaaaat	ttataatcag	aaaaataaat	attcaggagg	120

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ctcaccagaa gaataaagtg ctctgccagt tattaaagga ttactgctgg tgaattaaat      180
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aggattaact gttttaggaa cagatataaa gcttcgccac ggaagagatg gacaaagcac      300
aaagacaaca tgatacctta ggaagcaaca ctaccctttc aggcataaaa tttggagaaa      360
tgcaacatta tgcttcatga ataatatgta gaaagaaggt ctgatgaaaa tgacatcctt      420
aatgtaagat aactttataa gaattctggg tcaaataaaa ttctttgaag aaaacatcca      480
aatgtcattg acttatcaaa tactatcttg gcatataacc tatgaaggca aaactaaaca      540
aacaaaaagc tcacaccaa caaaaccatc aacttatttt gtattctata acatacgaga      600
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620

<210> 360

<211> 431

<212> DNA

<213> Homo sapien

<400> 360

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aaaaaaaaa agccagaaca acatgtgata gataatatga ttggctgcac acttccagac      60
tgatgaatga tgaacgtgat ggactattgt atggagcaca tcttcagcaa gagggggaaa      120
tactcatcat ttttggccag cagttgtttg atcaccaaac atcatgccag aatactcagc      180
aaaccttctt agctcttgag aagtcaaagt ccgggggaat ttattcctgg caattttaat      240
tggactcctt atgtgagagc agcggctacc cagctggggg ggtggagcga acccgctact      300
agtggacatg cagtggcaga gtccttggtt accacctaga ggaatacaca ggcacatgtg      360
tgatgccaa gctgacacct gtagcactca aatttgtctt gtttttgtct ttcgggtgtg      420
agattcttag t

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431

<210> 361

<211> 351

<212> DNA

<213> Homo sapien

<400> 361

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ttgggtcttc tggctctctt ccaagtttcc cagccactcg agggagaaat atcggggagg      180
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caatcctgga ttcaatgtct gaaacctcgc tctctgcttg ctggacttct gaggccgtca      300
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351

<210> 362

<211> 463

<212> DNA

<213> Homo sapien

<400> 362

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ccccggtcac agaaatgacc aggttgggtg ttttcagggt ccagtgtctg gtcagcagct      180
cgtaaaggat ttccgcgtcc gtgtcgcagg acagacgtat atacttccct ttcttcccca      240
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cacacttgca cacattctcc ctgataagca cgatgggtgt gacaggaagg aaggatttca      420
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463

<210> 363

<211> 653

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(653)

<223> n = A,T,C or G

<400> 363

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tgggaggcac tacgcaagat gggactgcgt cctggggtga gacatcctct ccttgagat	180
ctaacgaaac ttctcaccta tgagttgtaa agcagaaata cctgnactac agacgagtgc	240
ccaacagcaa cccccggaa gtatgagttc ctctrgggcc tccgttccta ccatgagasc	300
tagcaagatg naagtgttga gantcattgc agaggttcag aaaagagacc cntcgtgact	360
ggtctgcaca gttcatggag gctgcagatg aggccttggg tgctctggat gctgctgcag	420
ctgaggccga agccccggct gaagcaagaa cccgcattggg aattggagat gaggtgtgt	480
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attttggaga tccntgggtcc agaattccat ttaccttctg ggccagatac caccagaatg	600
ccgctccag attccctcag acctttgccg gtcccattat tggtcstggt ggt	653

<210> 364

<211> 401

<212> DNA

<213> Homo sapien

<400> 364

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aaaacaaggt ggatagatct agaattgtaa cattttaaga aaaccatagc atttgacaga	180
tgagaaagct caattataga tgcaaagtta taactaaact actatagtag taaagaaata	240
catttcacac ctttcatata aattcactat cttggcttga ggcaactccat aaaatgtatc	300
acgtgcatag taaatcttta tatttgctat ggcgttgac tagaggactt ggactgcaac	360
aagtggatgc gcggaaaatg aaatcttctt caatagccca g	401

<210> 365

<211> 356

<212> DNA

<213> Homo sapien

<400> 365

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atgtttcagt gctagagcgt aggaatagac cctggcgtcc actgtgagat gttcttcagc	120
taccagagca tcaagtctct gcagcaggtc attcttgggt aaagaaatga cttccacaaa	180
ctctccatcc cctggctttg gcttcggcct tgcgttttcg gcatcatctc cgtaaatggt	240
gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga	300
acattcggca atgtccctt tgtagccagt ttcttcttcg agtcccga gagcag	356

<210> 366

<211> 1851

<212> DNA

<213> Homo sapien

<400> 366

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ttgctgtttt	cagaagagat	ttttaacatc	tgtttttctt	tgtagtcaga	aagtaactgg	240
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cttttcccca	tttagtatta	tgttggctgt	gggcttgta	taggtgggtt	ttattacttt	1800
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<210> 367

<211> 668

<212> DNA

<213> Homo sapien

<400> 367

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accrtataag	agcagtgtct	tggccattaa	tttatctttc	atttgtagaca	gcrtagtgya	180
gagtggattt	tccatactca	tctggaatat	ttggatcagt	gccatgttcc	agcaacatta	240
acgcacattc	atcttctctg	cattgtacgg	cctgtcagta	ttagacccaa	aaacaaatta	300
catatcttag	gaattcaaaa	taacattcca	cagctttcac	caactagtta	tatttaaagg	360
agaaaactca	tttttatgcc	atgtattgaa	atcaaaccce	cctcatgctg	atatagttgg	420
ctactgcata	cctttatcag	agctgtcttc	tttttgttgt	caaggacatt	aagttgacat	480
cgtctgtcca	gcaggagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	540
gcagtcctat	gagagtgaga	agacttttta	ggaaattgta	gtgcactagc	tacagccata	600
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<210> 368

<211> 1512

<212> DNA

<213> Homo sapien

<400> 368

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tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tggtgctgcc	gttgcttccc	ctgctgcagg	cgagcggca	agagcaacgt	gggcacttct	360
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actccaagaa	aagttaaaca	tgtttcagtg	aatagagatc	ctgctccttt	ggcaagttcc	1440
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<210> 369

<211> 1853

<212> DNA

<213> Homo sapien

<400> 369

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<210> 370

<211> 2184

<212> DNA

<213> Homo sapien

<400> 370

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ctgcgcagc	ttcgggataa	cttgaggctg	catcactggg	gaagaaacac	aytctgtcc	360
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<210> 371
 <211> 1855
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(1855)
 <223> n = A,T,C or G

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 acatgtttca gtgaatagag atcctgctcc tttggcaagt tcctaaaaaa cagtaataga 1800
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<210> 372
 <211> 1059
 <212> DNA
 <213> Homo sapien

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 gcgcttgrgg agactmcgat gacagygcct tcatggagcc caggtaccac gtccgtggag 180
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 catctggcct ctgccaatgg gaattcagaa gtagtaaaac tcstgctgga cagacgatgt 360

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<210> 373

<211> 1155

<212> DNA

<213> Homo sapien

<400> 373

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<210> 374

<211> 2000

<212> DNA

<213> Homo sapien

<400> 374

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<210> 375

<211> 2040

<212> DNA

<213> Homo sapien

<400> 375

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<210> 376

<211> 329

<212> PRT

<213> Homo sapien

<400> 376

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Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
35           40           45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
50           55           60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
65           70           75           80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
85           90           95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
100          105          110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
115          120          125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
130          135          140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
145          150          155          160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
165          170          175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
180          185          190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
195          200          205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
210          215          220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225          230          235          240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
245          250          255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
260          265          270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
275          280          285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu

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<210> 377

<211> 148

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(148)

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<400> 377

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 35 40 45
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
 50 55 60
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
 65 70 75 80
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
 85 90 95
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
 100 105 110
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
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 130 135 140
 Lys Asn Lys Val
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<210> 378

<211> 1719

<212> PRT

<213> Homo sapien

<400> 378

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 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn

85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
 370 375 380
 Pro Arg Thr His Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser
 385 390 395 400
 Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys
 405 410 415
 Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly
 420 425 430
 Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys
 435 440 445
 Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly
 450 455 460
 Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys
 465 470 475 480
 Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys
 485 490 495
 Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp
 500 505 510
 Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu
 515 520 525

Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp
 530 535 540
 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln
 545 550 555 560
 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val
 565 570 575
 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn
 580 585 590
 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu
 595 600 605
 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp
 610 615 620
 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys
 625 630 635 640
 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys
 645 650 655
 Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
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 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
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 690 695 700
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 His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln
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 785 790 795 800
 Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly
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 820 825 830
 Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe
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 Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser
 850 855 860
 Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn
 865 870 875 880
 Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu
 885 890 895
 Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile
 900 905 910
 Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn
 915 920 925
 Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro
 930 935 940
 Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu
 945 950 955 960
 Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe

965 970 975
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 1075 1080 1085
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 Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys
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 1155 1160 1165
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 1235 1240 1245
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 1285 1290 1295
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 His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala
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 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
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 1490 1495 1500
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 1570 1575 1580
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
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 Met Lys His Gln Ser Gln Leu
 1715

<210> 379

<211> 656

<212> PRT

<213> Homo sapien

<400> 379

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 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60

Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
 450 455 460
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
 465 470 475 480
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
 485 490 495
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu

```

      500      505      510
Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys
      515      520      525
Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly
      530      535      540
Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser
545      550      555      560
Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr
      565      570      575
His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln
      580      585      590
Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln
      595      600      605
Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys
      610      615      620
Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile
625      630      635      640
Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
      645      650      655

```

```

<210> 380
<211> 671
<212> PRT
<213> Homo sapien

```

```

      <400> 380
Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1      5      10      15
Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
      20      25      30
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
      35      40      45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
      50      55      60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
65      70      75      80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
      85      90      95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
      100      105      110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
      115      120      125
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
      130      135      140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145      150      155      160
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
      165      170      175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
      180      185      190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
      195      200      205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
      210      215      220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn

```


<210> 381
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 381
 ggagaagcgt ctgctggggc aggaaggggt ttccctgccc tctcacctgt ccctcaccaa 60
 ggtaacatgc ttcccctaag ggtatcccaa cccaggggccc tcaccatgac ctctgagggg 120
 ccaatatccc aggagaagca ttggggagtt gggggcaggt gaaggaccca ggactcacac 180
 atcctggggc tccaaggcag aggagagggt cctcaagaag gtcaggagga aaatccgtaa 240
 caagcagtca g 251

<210> 382
 <211> 3279
 <212> DNA
 <213> Homo sapiens

<400> 382
 cttcctgcag ccccatgct ggtgaggggc acgggcagga acagtggacc caacatggaa 60
 atgctggagg gtgtcaggaa gtgatcgggc tctggggcag ggaggagggg tggggagtgt 120
 cactgggagg ggacatcctg cagaaggtag gagtgcagca acaccgctg caggggaggg 180
 gagagccctg cggcacctgg gggagcagag ggagcagcac ctgccaggc ctgggaggag 240
 gggcctggag ggcgtgagga ggagcagagg ggctgcattg ctggagttag ggatcagggg 300
 cagggcgctg gatggcctca cacagggaag agagggcccc tctgcaggg cctcacctgg 360
 gccacaggag gacactgctt ttctcttagg gagtgcaggag ctgtggatgg tgctggacag 420
 aagaaggaca gggcctggct cagggtgtcca gaggctgtcg ctggcttccc tttgggatca 480
 gactgcaggg agggagggcg gcagggttgt ggggggagtg acgatgagga tgacctgggg 540
 gtggctccag gccttgcccc tgccctgggc ctcacccagc ctccctcaca gtctcctggc 600
 cctcagctc tcccctccac tccatcctcc atctggcctc agtgggtcat tctgatcact 660
 gaactgacca taccagccc tgcccacggc cctccatggc tccccaatgc cctggagagg 720
 ggacatctag tcagagagta gtccctgaaga ggtggcctct gcgatgtgcc tgtgggggca 780
 gcacctcgca gatggtcccg gccctcatcc tgctgacctg tctgcaggga ctgtcctcct 840
 ggaccttgcc ccttgtgcag gagctggacc ctgaagtccc ctcccatag gccaagactg 900
 gagccttgtt cctctgttg gactccctgc ccatattctt gtgggagtgg gttctggaga 960
 catttctgtc tgttcttagg agctgggaat tgctctcagt catctgcctg cggggttctg 1020
 agagatggag ttgcctaggc agttattggg gccaatcttt ctactgtgt ctctcctcct 1080
 ttacccttag ggtgattctg ggggtccact tgtctgtaat ggtgtgcttc aaggtatcac 1140
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 gcattaccgg aagtggatca aggacaccat cgcagccaac ccctgagtgc ccctgtccca 1260
 cccctacctc tagtaaat t aagtccacct caggttctgg catcacttgg cctttctgga 1320
 tgctggacac ctgaagcttg gaactcacct ggccgaagct cgagcctcct gagtccctact 1380
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 tgtttgtggg gtgcagagat gggaggggtg gggccacccc tgggaagagtg gacagtga 1620
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 acacacagca aggttgacgc tgtaaacata gccacgctg tctggggggc actgggaagc 1740
 ctagataagg ccgtgagcag aaagaagggg aggatcctcc tatgttgttg aaggagggac 1800
 tagggggaga aactgaaagc tgattaatta caggaggttt gttcaggtcc cccaaaccac 1860
 cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtggt 1920
 ttattatggt ttgttacatt gataggatac atactgaaat cagcaaaca aacagatgta 1980
 tagattagag tgtggagaaa acagaggaaa acttgacgtt acgaagactg gcaacttggc 2040
 ttactaagt tttcagactg gcaggaagtc aaacctatta ggctgaggac cttgtggagt 2100
 gtagctgac cagctgatag aggaactagc cagggtgggg cctttccctt tggatggggg 2160

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gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataaatatg tacaaagtaa ttccaactga ggaagctcac ctgaccccta 2280
gtgtccaggg tttttactgg gggctctgtag gacgagtatg gagtacttga ataattgacc 2340
tgaagtcctc agacctgagg ttccctagag ttcaaacaga tacagcatgg tccagagtcc 2400
cagatgtaca aaaacaggga ttcatcacia atcccatctt tagcatgaag ggtctggcat 2460
ggccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaatgtc 2520
atctcccagg agttattcaa gggtagagccc tttacttggg atgtacaggc tttgagcagt 2580
gcagggtctgc tgagtcaacc ttttattgta caggggatga gggaaaggga gaggatgagg 2640
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aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcctt cttttcacac cattgggtgag ggagggatta ccaccttggg 2820
gttatgaaga tgggtgaaca cccacacat agcaccggag atatgagatc aacagtttct 2880
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gttttgagac tggcaggtag tgaaactcat taggctgaga accttgtgga atgcagctga 3120
cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaaa aaaagttttt 3279

```

<210> 383

<211> 155

<212> PRT

<213> Homo sapiens

<400> 383

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Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
      5                      10                      15

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
      20                      25                      30

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
      35                      40                      45

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
      50                      55                      60

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
      65                      70                      75                      80

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
      85                      90                      95

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
      100                     105                     110

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
      115                     120                     125

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
      130                     135                     140

Ala Leu Glu Arg Gly His Leu Val Arg Glu
      145                     150

```

<210> 384
<211> 557
<212> DNA
<213> Homo sapiens

<400> 384
ggatcctcta gagcgccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60
aaagatgtgt tttgttttgg actctctgtg gtcccttcca atgctgtggg tttccaacca 120
ggggaagggt cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggg 180
tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240
acttaacctt gaaatggaaa gtcttgcaat ccattttgca ggatccgtct gtgcacatgc 300
ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360
tccccaagac acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420
ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaagt 480
tcaattgtga aaatgaatat catgcaaata aattatgcga ttttttttcc aaagtaaaaa 540
aaaaaaaaa aaaaaaa 557

<210> 385
<211> 337
<212> DNA
<213> Homo sapiens

<400> 385
ttcccagggt atgtgcgagg gaagacacat ttactatcct tgatggggct gatcccttta 60
gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120
tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
tatcagacag gtccagtttc cgcaccaaca cctgctggtt ccctgtcgtg gtctggatct 300
ctttggccac caattcccc ttttccacat cccggca 337

<210> 386
<211> 300
<212> DNA
<213> Homo sapiens

<400> 386
gggcccgtca ccggcccagg ccccgccctcg cgagtcctcc tccccgggtg cctgcccgcga 60
gcccgtcctg ccagagggtt gggcgcgggg ctgcctctac cggctggcgg ctgtaactca 120
gcgaccttgg ccggaaggct ctagcaagga ccacccgacc ccagccgagg cggcggcggc 180
gcggactttg cccggtgtgt ggggcggagc ggactgctgt tccgcggacg ggcagcgaag 240
atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

<210> 387
<211> 537
<212> DNA
<213> Homo sapiens

<400> 387
gggcccagtc gggcaccaag ggactctttg caggcttcct tctcggatc atcaaggctg 60
ccccctcctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120
tgaaccagga ccggcttctg ggcggctgaa aggggcaagg aggcaaggac ccgctctctc 180
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttcctc agcactgagg 240
gagggggcct gtttcccttc cctcccggcg acaagctcca gggcagggct gtccctctgg 300

```
gcggcccagc acttcctcag acacaacttc ttcctgctgc tccagtcgtg gggatcatca 360
cttaccaccacc ccccaagttc aagaccaaata cttccagctg ccccttcgt gttccctgt 420
gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctcagcctgg ttagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaaa aaaaaaa 537
```

<210> 388

<211> 520

<212> DNA

<213> Homo sapiens

<400> 388

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aggataatTT ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgagggttaaa ccagtttgca tccccctaata gtggaaaaag taagaggact actcagcact 120
gtttgaagat tgccctctct acagcttctg agaatttgtt tatttcactt gccaaagtga 180
ggacccccctc cccaacatgc cccagcccac ccctaagcat ggtcccttgt caccaggcaa 240
ccaggaaact gctacttggt gacctcacca gagaccagga gggtttggtt agctcacagg 300
acttccccca cccagaaga ttagcatccc atactagact cactactcaac tcaactaggc 360
tcataactcaa ttgatgggta ttagacaatt ccatttcttt ctgggttatta taaacagaaa 420
atctttcttc ttctcattac cagtaaaggc tcttggtatc tttctgttgg aatgatttct 480
atgaacttgt cttattttaa tgggggggtt ttttctgtgt 520
```

<210> 389

<211> 365

<212> DNA

<213> Homo sapiens

<400> 389

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cgttgccccg gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagttaaggc tggatttcag atctgcctgg ttccagccgc agtgtgccct ctgctcccc 120
aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgct ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ccttctctct ccttcagcaa ggggcgttgc ccacattctc 300
tgagggtcag tggagaagcc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365
```

<210> 390

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(221)

<223> n = A,T,C or G

<400> 390

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tgccctctca tcttgcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacggntt ctcatgggtg tggaaacatct ctgcttgagg ttccaggaag gcctctggct 120
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221
```

<210> 391

<211> 325

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(325)
<223> n = A,T,C or G

<400> 391
tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
ctctcgcgcc cagcctggag ctgctcctgg catctaccaa caatcagncg aggcgagcag 120
tagccagggc actgctgcca acagccagtc cnnataccat catgtnaccc ggtgngctct 180
naanttn gat ntccanagcc ctacccatcn tagttctgct ctcccacccg ntaccagccc 240
cactgcccag gaatcctaca gccagtaccc tgtcccgacg tctctaccta ccagtacgat 300
gagacctccg gctactacta tgacc 325

<210> 392
<211> 277
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(277)
<223> n = A,T,C or G

<400> 392
atattgttta actccttctt ttatatcttt taacattttc atggngaaaag gttcacatct 60
agtctcactt nggcnagn gn ctctacttg agtctcttcc ccggcctggn ccagtnghaa 120
antaccanga accgncatgn cttaanaacn ncctggtttn tgggttnntc aatgactgca 180
tgagtgacac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcg 240
ctgaggatac agcgcgcgt cctgtgttg tggggaa 277

<210> 393
<211> 566
<212> DNA
<213> Homo sapiens

<400> 393
actagtccag tgtggtggaa ttcgcgccg cgtcgacgga caggtcagct gtctggctca 60
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga tttaaattcag cctaaacgtt 120
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgccccga 180
gagaaggctc agtttgcca tcagcattat catgatatac ggactgggta cttgggttaag 240
gaggggtcta ggagatctgt cccttttaga gacaccttac ttataatgaa gtatttgga 300
gggtgggttt caaaaagtaga aatgtcctgt attccgatga tcctcctgta aacattttat 360
catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420
ttctgcctca atgtttactg tgcctttgtt tttgctagtt tgtgtgtgtg aaaaaaaaaa 480
cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540
ttttgcctat caaaaaaaaa aaaaaa 566

<210> 394
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(384)

<223> n = A,T,C or G

<400> 394

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gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaattng gaccggggcca aggctggact gctggagcgt gtgaaggagc tacagggcna 120
gcaggaggac cgggctttaa ggagttttaa gctgagtgct actgtagacc ccaaatacca 180
tcccaagatt atcgggagaa agggggcagt aattacccaa atccgggttg agcatgacgt 240
gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
tgagcagatg gtttctgagg acgt                                     384
```

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

```
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgc 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcattcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc atgggacggg 360
gcagcctggg gagaccatcc aatcccaaat aaaatgcac                                     399
```

<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

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tggagttntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaaa gtggatgaat aatctggata ttttccctaa aaagattcct tgaaacacat 240
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gttttagggga gggagtgagg gataaaagaa ggaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt                                     403
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<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397

actagtnacg tgtgggtggaa ttcgcggccg cgtcgacctt naanccatct ctatagcaaa 60
tccatccccg ctcttggttg gtnacagaat gactgacaaa 100

<210> 398

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 398

gcggccgcgt cgacagcagt tccgccagcg ctgcgccctg ggtggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

<210> 399

<211> 298

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(298)

<223> n = A,T,C or G

<400> 399

acggagggtg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
gggggtgccng catggagcgc atgggcgcgg gcctggggcca cggcatggat cgcgtgggct 120
ccgagatcga gcgcattggc ctgggtcatgg accgcatggg ctccgtggag cgcattgggct 180
ccggcattga gcgcattggc ccgctgggcc tcgaccacat ggctccanc attgancgca 240
tgggccagac catggagcgc attgggtctg gcgtggagcn catgggtgcc ggcatggg 298

<210> 400

<211> 548

<212> DNA

<213> Homo sapiens

<400> 400

acatcaacta ctctctcatt ttaaggtagt gcagttccct tcatcccctt ttcctgcctt 60
gtacatgtac atgtatgaaa tttccttctc ttaccgaact ctctccacac atcacaaggt 120
caaagaacca cagccttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt ttttccacgt ttaaggggcc atggcaggac ttagagttgc gagttaagac 240
tgacagaggc tagagaatta tttcatacag gctttgaggc caccatgtc acttatcccg 300
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
gttggcccca taattctggg cctttgttgt ttgttttaat tacttgggca tcccaggaag 420
ctttccagtg atctctacc atgggcccc ctctgggat caagcccc cccaggccctg 480
tcccagccc ctctgcccc agcccaccg cttgccttgg tgctcagccc tccattggg 540
agcaggtt 548

<210> 401
<211> 355
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(355)
<223> n = A,T,C or G

<400> 401
actgtttcca tgttatgttt ctacacattg ctacctcagt gctcctggaa acttagcttt 60
tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120
taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
tataaatgaa tgtgctgaag caaagtgcc atggtggcgg cgaagaagan aaagatgtgt 240
tttgttttgg actctctgtg gtcccttcca atgctgnngg tttccaacca ggggaagggt 300
cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggn tctgc 355

<210> 402
<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(407)
<223> n = A,T,C or G

<400> 402
atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60
tctcacatgc ggtggcatatc ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120
aaatggaaaa cagaaaaaag cagggtgttg actcctactt tctgacaaaa cagactatgc 180
gaataaagat aaaaaagaga aggacattac aaaggtgggc ctgacctttg ataaatctca 240
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300
ttgtggagct tctccctgac agagagtccc tgatctccca aaatttggtt gagatgtaag 360
gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407

<210> 403
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 403
cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaatcc aggcacaaaa 60
tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120
tagagaacaa gacctactca gtcattgaaca aaaaggcaga caccaacatg gatctcatgg 180
gggattggat attgtaatta tagagcagga agatgacagt gatcgctatt tggcacaaca 240
tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300
gga 303

<210> 404
<211> 225
<212> DNA
<213> Homo sapiens

<400> 404
aagtgttaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60
attgtttaatg cactcattta cctttacatg gtgaaagtgc tctcttgatc ctacaaacag 120
acattttcca ctctgtgttc catagtgtt aagtgtatca gatgtgttg gcatgtgaat 180
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(334)
<223> n = A,T,C or G

<400> 405
gagctgttat actgtgagtt ctactaggaa atcatcaaatt ctgaggggtg tctggaggac 60
ttcaatacac ctccccccat agtgaatcag cttccagggg gtccagtcct tctccttact 120
tcatcccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggc 180
ttcccagtg ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtg 240
ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgc cagcccatgt 300
cactctccac tctctcannng tggatccac ccct 334

<210> 406
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(216)
<223> n = A,T,C or G

<400> 406
tttcatacct aatgaggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
acnaaacaca aattttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
actgccaaag aatnttcaag aaggaggact gccant 216

<210> 407
<211> 413
<212> DNA
<213> Homo sapiens

<400> 407
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
gtacaacatt gcaccagtg tcagattcta cacctggcca ctgaggaagc aagagttaat 180
ccagagggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240

ggaaaattgt catttgcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt ttctctgtca 360
tgggagttcc agaaaaagtt aaaacagaca atgggccagg ttctgtagta aag 413

<210> 408

<211> 183

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(183)

<223> n = A,T,C or G

<400> 408

ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tnccttaacta gttaatcctt aaagggtan ntaatcctta actagtcctt ccattgtgag 120
cattatcctt ccagtattcn cttctnttt tatttactcc ttcttggtta cccatgtact 180
ntt 183

<210> 409

<211> 250

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(250)

<223> n = A,T,C or G

<400> 409

cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60
gtggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
gcttcccagt gccccagga cagcgtgggc tatgtttaca gcgntcctt gctggggggg 240
ggcctatgc 250

<210> 410

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(306)

<223> n = A,T,C or G

<400> 410

ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tcccatgtgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120
cccagggacc ttggaaacag ttggcactgt aagggtgctt ctccccaaaga cacatcctaa 180
aagggtgttg aatggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240
nactggttgg ctttttttgn atctttttta aactggaaaag ttcaattgng aaaatgaata 300
tcntgc 306

<210> 411
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G

<400> 411
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggngaggcaa a 261

<210> 412
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 412
gttcaatgtt acctgacatt tctacaacac cccactcacc gatgtattcg ttgcccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgcccagg aaatactacg 120
actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
ctggggagatt tcactgggta cattgaattc caaaactacc cangcaatta cccagccaac 240
a 241

<210> 413
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(231)
<223> n = A,T,C or G

<400> 413
aactcttaca atccaagtga ctcatctgtg tgcttgaatc cttccactg tctcatctcc 60
ctcatccaag tttctagtac cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120
aagtttactc tcctcatttg gaacctaaaa actctcttct tcctgggtct gagggctcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414
<211> 234
<212> DNA
<213> Homo sapiens

<400> 414
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt ctccctttgg catgggatgg ggatgaagta aggagaggga 180
ctggaccccc tggaaagtga ttcactatgg ggggagggtg attgaagtcc tcca 234

<210> 415
<211> 217
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(217)
<223> n = A,T,C or G

<400> 415
gcataggatt aagactgagt atcttttcta cattctttta acttttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttctca 120
cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggt tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc 217

<210> 416
<211> 213
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(213)
<223> n = A,T,C or G

<400> 416
atgcatatnt aaagganact gcctcgcttt tagaagacat ctggngctgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag 213

<210> 417
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 417
nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
gtgggaaagg ctttactctg agttcaaadc ttcaagccca tcagagagtc cacactggag 120
agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240
tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300
agt 303

<210> 418
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 418
tttttggcgg tgggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60
tgcacaggca tgatctcggc tcactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacacca gctagttttt 180
gtatttttag tagagacagg gtttcacat gttggccagg ctggtctcaa actcctnacc 240
tcagnngtca ggctggctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300
aaagtgctan gattacaggc cgtgagcc 328

<210> 419
<211> 389
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

<400> 419
cctctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatag 60
accctgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgtttcct ctctgtggct ccattcatag cacagtgtt gcactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggt gtgccaggca 240
ccggttctcc agccaccaac ctactcgtc cccgcaaag gcacatcagt tcttctaccc 300
taaaggtagg accaaaggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360
tggcagccac tcnggctgtg tcgacgcgg 389

<210> 420
<211> 408
<212> DNA
<213> Homo sapiens

<400> 420
gttcctccta actcctgcc aaaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtc tcttgtttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtgtg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgtatg aaaaacctgg caagcccg 408

<210> 421
<211> 352
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(352)

<223> n = A,T,C or G

<400> 421

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gctcaaaaat ctttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacaggtct tttttgggtc cttcttctcc accacnata acttgagtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacaggtg tagaaacaag 240
gggtgcaacat gaaatttctg tttcgtagca agtgcagtgc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg 352
```

<210> 422

<211> 337

<212> DNA

<213> Homo sapiens

<400> 422

```
atgccaccat gctggcaatg cagcggggcg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgccggcg atcgcggcgg cgtcaatcct ggccaaggtc agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcgggcgg cataagggtc 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgcc attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat 337
```

<210> 423

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(310)

<223> n = A,T,C or G

<400> 423

```
gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
aggagaatga ggcctggcct gggagccctg tgctactan aagcncatta gattatccat 120
tcactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180
tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300
tccgagttta 310
```

<210> 424

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(370)

<223> n = A,T,C or G

<400> 424

```
gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
cactgacaga acaggctctt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180
ccttcttgaa gattcttttg cagttgtcct tgtcataacc cacaggtgta gaaacatcct 240
ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
cacgaagggt gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
tccgtcgacg                                     370
```

<210> 425

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(216)

<223> n = A,T,C or G

<400> 425

```
aattgctatn ntttattttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaataga 60
taacaacnca acatcaagg n aaananaaca ggaatggntg acnttgcata aatnggccga 120
anattatcca ttatnttaag ggttgacttc aggntacagc acacagacaa acatgcccag 180
gaggntntca ggaccgctcg atgtnttntg aggagg                                     216
```

<210> 426

<211> 596

<212> DNA

<213> Homo sapiens

<400> 426

```
cttccagtga ggataaccct gttgccccgg gccgagggtc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gccccagggt tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatggtga 180
gctgtccttg tattttgatt aacctaattg ccttcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggcca ttaagaggca cttcccgtta 300
ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
ggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggtc tactgcctga 540
gtcccgcgtg tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct     596
```

<210> 427

<211> 107

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(107)

<223> n = A,T,C or G

<400> 427

```
gaagaattca agtttaggttt attcaaaggg cttacngaga atcctanacc caggncccag 60
```

```

cccgggagca gccttanaga gctcctgttt gactgcccgg ctcagng
107

<210> 428
<211> 38
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(38)
<223> n = A,T,C or G

<400> 428
gaacttcena anaangactt tattcactat ttacatt
38

<210> 429
<211> 544
<212> DNA
<213> Homo sapiens

<400> 429
ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
tttggatggt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240
gccttccact tcagttacac ctcaactcacc atcctctcct gttgggttctg tgctgcttca 300
agatactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
tgatgtgcag ttataaaaatc tgccctttta tgatgtcctt gatgttctca tcaagccac 420
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
acctcaacaa gtttagagaga tatgcatac cagggatttt ttgccagggt gtaggagaga 540
ttat
544

<210> 430
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(507)
<223> n = A,T,C or G

<400> 430
cttatcncaa tggggctccc aaacttggt gtgcagtga aactccgggg gaattttgaa 60
gaacactgac acccatcttc caccgccgaca ctctgattta attgggctgc agtgagaaca 120
gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttggt atctttgccn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgagggg gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcgtggt ggagaagaag gacccaaaaa agacctgttc 360
tgtcagtga tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
cattctctc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa
507

<210> 431
<211> 392

```

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 431

```
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcctgggtt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggcttttac tctgctgttt ct 392
```

<210> 432

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(387)

<223> n = A,T,C or G

<400> 432

```
ggtatcanta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcgna gtccagccac tngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgtgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgta aggaccggga 360
acaacgtata gaacactgga gtccttt 387
```

<210> 433

<211> 281

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(281)

<223> n = A,T,C or G

<400> 433

```
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagnaggg ntctctgtnt gccactgggt 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281
```

<210> 434

<211> 484

<212> DNA

<213> Homo sapiens

<400> 434

```
ttttaaaata agcatttagt gctcagtcct tactgagtag tctttctctc ccttcctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120
tgttgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtaga tccatcttgc 180
tttttccccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatgggtc tcagaacccat ttcacccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccc 360
tgctccaate tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480
ttta
```

<210> 435

<211> 424

<212> DNA

<213> Homo sapiens

<400> 435

```
gcgcgcgtca gagcaggtca ctttctgcct tccacgtcct ccttcaagga agccccatgt 60
gggtagcttt caatctgca ggttcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaacccc ctccctcgcc gacttcggaa ctggcgagag ttcagcgag 180
atgggcctgt ggggaggggg caagatagat gagggggagc ggcattggtc ggggtgaccc 240
cttgagagaga ggaaaaaggc cacaagaggg gctgccaccg ccaactaacg agatggccct 300
ggtagagacc tttgggggtc tggaaacctt ggactcccca tgctcttaact cccacactct 360
gctatcagaa acttaaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac
```

424

<210> 436

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(667)

<223> n = A,T,C or G

<400> 436

```
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattcctc tgatttcaaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggtg tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
gccaggtttg tcatagcact catcaaagtc cgggtcaacgt ctgtgcttcg aatataaacc 360
tgttcattgt tataggactc attcaagaat tttctatata tctttcttat atactctcca 420
agttcataat gctgctccat gccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tgggggtcagt gggaaagggt tcaatgggac ttcgggtctcc atgccgaaac 540
accaaagtca caaacttcaa ctcttggtc agtacacttc ggtctagcca gaaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660
tgttgag
```

667

<210> 437

<211> 693

<212> DNA

<213> Homo sapiens

<400> 437

```
ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaaag ctggattggc acactaggac tctaccatac cgggttttgt 120
taaagctcag gttaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
ataaaagata attccttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtaactct ctatcttcac cctcttgct tctactctct ggcagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttggggggac agccagcctc tttagctttc 420
atctgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaaact gctgttgctc ctgaggtggt gaaagacaga tatagagctt acagtattta 540
tcctatttct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc                                     693
```

<210> 438

<211> 360

<212> DNA

<213> Homo sapiens

<400> 438

```
ctgcttatca caatgaatgt tctcctgggc agcgttgtga tctttgccac ctctgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaaag acaactgcca aagaatcttc aagaaggagg 180
actgcaagta tatctgggtg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagc ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360
```

<210> 439

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 439

```
gttcctnnta actcctgcc a gaaacagctc tctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag t                                     431
```

<210> 440

<211> 523

<212> DNA

<213> Homo sapiens

<400> 440
agagataaag cttaggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tattaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaagtgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttacccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcttggaaac tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaat acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta 523

<210> 441

<211> 430

<212> DNA

<213> Homo sapiens

<400> 441
gttctctcta actcctgcc aaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttggttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagttag tgactttggg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatattagtag 430

<210> 442

<211> 362

<212> DNA

<213> Homo sapiens

<400> 442
ctaaggaatt agtagtggtc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcttgtaa tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180
atgtttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc 362

<210> 443

<211> 624

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(624)

<223> n = A,T,C or G

<400> 443
tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240


```
cccaaacac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaataaac 360
taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtac 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatc 624
```

<210> 444

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(425)

<223> n = A,T,C or G

<400> 444

```
gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgttg gtcagcaaat ccttgaatgc 180
tgcttaatgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcacctgt gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggctcgacg cggccgcgaa tttagtagta 420
gtaga 425
```

<210> 445

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 445

```
catgtttatg nttttggatt actttgggca cctagtgttt ctaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcatgtggc agattattgg atgtagtctt ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggccttctc tcttgtattt tgaagcagtg 360
tggtgtctgg attgataaaa aaaaaaaaaa tgcacgcggc cgcaattta gtag 414
```

<210> 446

<211> 631

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(631)

<223> n = A,T,C or G

<400> 446

```

acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcagggtgtg 120
atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtgggtggtc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaaactttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatgtt tcacagtggc tggactaccg agagcttggg ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgcttg catttgtggt 540
aatctacacc aatgaaaaca tgtactacag ctatatattga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g

```

631

<210> 447

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(585)

<223> n = A,T,C or G

<400> 447

```

ccttgggaaa antntcacia tataaagggg cgtagacttt actccaaatt ccaaaaaggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagtctctga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat ctccagaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggtcg 300
ccagggttct catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaaggtgt caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttgggta gtacacttcg gtcta

```

585

<210> 448

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(93)

<223> n = A,T,C or G

<400> 448

```

tgctcgtggg tcattctgan nnccgaactg acctgcccag ccctgccgan gggccnccat 60
ggctccctag tgccctggag agganggggc tag

```

93

<210> 449

<211> 706

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(706)
 <223> n = A,T,C or G

<400> 449
 ccaagttcat gctntgtgct ggacgctgga cagggggcaa aagcnnttgc tcgtgggtca 60
 ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120
 cctggagagg aggtgtctag tcagagagta gtccctggaag gtggcctctg ngaggagcca 180
 cggggacagc atcctgcaga tggtcgggcg cgtcccatc gccattcagg ctgcgcaact 240
 gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
 gtgctgcaag gcgattaagt tgggtaacgc caggggttttc ccagtcncga cgttgtaaaa 360
 cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcattgcacg 420
 cgtacgtaag cttggatcct ctagagcggc cgcctactac tactaaattc gcggccgcgt 480
 cgacgtggga tccnactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
 cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
 aacaggttga acctgggagg tggagggtgc aatgagctga gatcaggccn ctgcncccca 660
 gcatggatga cagagtgaag ctccatctta aaaaaaaaaa aaaaaa 706

<210> 450
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 450
 gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
 acagttttta aaggtaaaac aacataaaaa gaaatatect atagtggaaa taagagagtc 120
 aaatgaggct gagaacttta caaagggatc ttacagacat gtcgccaata tcaactgcatg 180
 agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240
 caagtcagggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
 agagacactg tcagagagtt aaaaagttag ttctatccat gaggtgattc cacagtcttc 360
 tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
 tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggt cgacgcggcc 480
 gcgaatttag tag 493

<210> 451
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(501)
 <223> n = A,T,C or G

<400> 451
 gggcgcgctc cattcgccat tcaggctgcg caactgttgg gaagggcgat cgggtgcgggc 60
 ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
 aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
 tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
 gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300
 tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacaa 360
 cgcncagac actcacagct actcaggagg ctgagaacag gttgaacctg ggagggtggag 420
 gttgcaatga gctgagatca ggccnctgcn ccccgacatg gatgacagag tgaaactcca 480

tcttaaaaaa aaaaaaaaaa a

501

<210> 452

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(51)

<223> n = A,T,C or G

<400> 452

agacggtttc accnttataa cnccttttag gatgggnntt ggggagcaag c

51

<210> 453

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(317)

<223> n = A,T,C or G

<400> 453

tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60
 acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaacct 120
 ttcacccana cagcctgttt ctatcctgtt taataaatta gtttgggtc tctacatgca 180
 taacaaaccc tgtccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240
 cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300
 taccatgtc tttatta 317

<210> 454

<211> 231

<212> DNA

<213> Homo sapiens

<400> 454

ttcgaggtag aatcaactct cagagtgtag tttccttcta tagatgagtc agcattaata 60
 taagccacgc cagctcttg aaggagtctt gaattctcct ctgtcactc agtagaacca 120
 agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180
 cttcctttt tcagtgttcc aaagctctc acaatttcat gaacaacagc t 231

<210> 455

<211> 231

<212> DNA

<213> Homo sapiens

<400> 455

taccaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60
 cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120
 gtttcaacgc attgatgact tctccaagga ttttcttttg gcatcgacca cattcagggg 180
 caaagaattt ctcatagcac agtcacaaat acagggtctc ttttctctct a 231

<210> 456
<211> 231
<212> DNA
<213> Homo sapiens

<400> 456
ttggcaggta cccttacaaa gaagacacca taccttatgc gttattaggt ggaataatca 60
ttccattcag tattatcggt attattcttg gagaaaccct gtctgtttac tgtaaccctt 120
tgcactcaaa ttccctttatc aggaataact acatagccac tatttacaaa gccattggaa 180
cctttttatt tgggtgcagct gctagtcagt ccctgactga cattgccaag t 231

<210> 457
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(231)
<223> n = A,T,C or G

<400> 457
cgaggtagcc aggggtctga aaatctctnn tttantagtc gatagcaaaa ttgttcatca 60
gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catacagttt 120
tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231

<210> 458
<211> 231
<212> DNA
<213> Homo sapiens

<400> 458
aggtctggtt cccccactt ccactccct ctactctctc taggactggg ctgggccaag 60
agaagagggg tggtaggga agccgttgag acctgaagcc ccaccctcta ccttccttca 120
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
ggtcctgggt taggcatttt ggggggccag accccaggag aagaagattc t 231

<210> 459
<211> 231
<212> DNA
<213> Homo sapiens

<400> 459
ggtaccgagg ctcgctgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60
ccttcgcgaa acctgtggtg gccaccagt cctaacggga caggacagag agacagagca 120
gccctgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460
<211> 231
<212> DNA
<213> Homo sapiens

<400> 460

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cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
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<210> 461

<211> 231

<212> DNA

<213> Homo sapiens

<400> 461

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gtggggttca gtgaggagtg ggaaattggt tcagcagaac caagccgttg ggtgaataag 180
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<211> 231

<212> DNA

<213> Homo sapiens

<400> 462

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gaagaactgt tagagagacc aacagggtag tgggttagag atttccagag tcttacattt 180
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<210> 463

<211> 231

<212> DNA

<213> Homo sapiens

<400> 463

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catttgacag gtgtcttttc ctctggacct cgggtgtccc atctgagtga gaaaaggcag 180
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<210> 464

<211> 231

<212> DNA

<213> Homo sapiens

<400> 464

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cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
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<210> 465

<211> 231

<212> DNA

<213> Homo sapiens

<400> 465

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aggatggcac aatTTTTgct tgtgttcata atatactcag attagttcag ctccatcaga 180
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<210> 466

<211> 231

<212> DNA

<213> Homo sapiens

<400> 466

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cctgtgcaat caaatattgt ggagaattcc ctagtggag aagtcacaaa gactataggc 180
aataatggag accagtccca caagatgaca accagtcgtt gtgtgcggct g 231
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<210> 467

<211> 311

<212> DNA

<213> Homo sapiens

<400> 467

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gcatgggtct ctgcccaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt 240
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<210> 468

<211> 3112

<212> DNA

<213> Homo sapiens

<400> 468

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<210> 469

<211> 2229

<212> DNA

<213> Homo sapiens

<400> 469

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2229

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<210> 470

<211> 2426

<212> DNA

<213> Homo sapiens

<400> 470

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2426

<210> 471

<211> 812

<212> DNA

<213> Homo sapiens

<400> 471

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812

<210> 472

<211> 515

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> n = A,T,C or G

<400> 472

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